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GenCore version 5.1.9
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- protein search, using sw model OM protein August 24, 2006, 01:16:00; Search time 194 Seconds (without alignments) 1121.830 Million cell updates/sec Run on:

US-10-679-362-2

Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2589679 Total number of hits satisfying chosen parameters:

2589679 segs, 457216429 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_8:\* Database :

geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2002s:\* geneseqp2002s:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2005s:\* geneseqp2006s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. n

# SUMMARIES

|        | Description  | Adf90164 Human tra | Adr03799 Human nov | Abg75834 Transport | Abp96441 Human tra | Abu52588 Human NOV | Aao14191 Human tra | Abu52587 Human NOV | Abb76941 Human VG5 | Adf90169 Human tra | Adr03804 Human hom | Ada55508 Human pro | Ads11015 Human the | Abp96446 Rat LYAAT | Abp96443 Mouse tra | Abb76935 Rat VG51. | Abb76934 Rat VG41. | Abb98199 Human HIP | Abp96437 Human tra | Aae26625 Human tra | Adn33124 Human tra | Aae29907 Human tra | Adq65947 Novel hum | Abp96435 Mouse tra |
|--------|--------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|        | ID           | ADF90164           | ADR03799           | ABG75834           | ABP96441           | ABU52588           | AA014191           | ABU52587           | ABB76941           | ADF90169           | ADR03804           | ADA55508           | ADS11015           | ABP96446           | ABP96443           | ABB76935           | ABB76934           | ABB98199           | ABP96437           | AAE26625           | ADN33124           | AAE29907           | ADQ65947           | ABP96435           |
|        | DB           | 7                  | œ                  | 9                  | 9                  | 9                  | Ŋ                  | 9                  | 4                  | 7                  | ထ                  | 9                  | 8                  | 9                  | ø                  | 4                  | 4                  | 2                  | 9                  |                    | 80                 | 9                  | 80                 | 9                  |
|        | Match Length | 476                | 476                | 507                | 476                | 496                | 568                | 200                | 476                | 476                | 476                | 434                | 434                | 475                | 475                | 475                | 382                | 483                | 483                | 483                | 483                | 507                | 483                | 478                |
| ا<br>ع | Match        | 100.0              | 100.0              | 99.9               | 99.7               | 9.66               | 97.3               | 97.1               | 94.1               | 94.1               | 94.1               | 89.8               | 89.8               | 86.9               | 86.9               | 86.8               | 8.69               | 69.8               | 8.69               | 9.69               | 9.69               | 9.69               | 69.4               | 68.7               |
|        | Score        | 2469               | 2469               | 2466               | 2461               | 2460               | 2402.5             | 2398               | 2324               | 2324               | 2324               | 2217               | 2217               | 2146.5             | 2144.5             | 2142.5             | 1723               | 1722.5             | 1722.5             | 1718.5             | 1718.5             | 1718.5             | 1713.5             | 1696.5             |
| 41.000 | Nesur.       | -                  | N                  | m                  | 4                  | ß                  | 9                  | 7                  | 80                 | 6                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 |

The invention describes an isolated peptide comprising a 476 amino acid sequence (S1) or its allelic variant, orthologue or fragment, where the allelic variant or orthologue is encoded by a nucleic acid that hybridises under stringent conditions to the opposite strand of a nucleic acid comprising a sequence having 2093 or 46649 base pairs, and the fragment comprises 10 contiguous amino acids of S1. The peptide is useful for preparing a composition for treating a disease or condition mediated

|           |         |         |         |          |         |         |          |          |          |          |          |          |          |          |          |          |           | ٠,                 |          |          |          |          |
|-----------|---------|---------|---------|----------|---------|---------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-----------|--------------------|----------|----------|----------|----------|
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| Dat trand | 00000   | Ī       | Human   | Human    | Нишап   | Human   | Human    | Human    | Mouse    | Human    | Novel    | Rat VG   | Human    | Human    |          | Amino    | nan       | umar               | Human    | Human    | Human    | Human    |
|           |         |         |         |          |         |         |          |          |          |          |          |          |          |          |          |          |           | H<br>9             |          |          |          |          |
| Ahn96436  | 2500000 | 200     | 7216    | 5438     | 3715    | 9500    | Adp29656 | Aae25571 | Abp96442 | Ads11014 | Adq67776 | 5931     | Abu52589 | Ads12237 | Ads12238 | Abb99355 | Add37511  | 1885               | Aam38898 | Adn95120 | Aam40684 | Aae04910 |
| hn 9      | 7,4     | 200     | dj2.    | pb3(     | dro     | dp2     | dp2      | ae2      | pb3(     | ds1      | gdę.     | pp.      | bu5;     | ds1      | ds1      | pp3      | gg3.      | Aef:               | am38     | du9      | ат4 (    | ae0      |
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| 96790000  | 00000   | 2202    | ADJ2721 | ABP96438 | ADR0971 | ADP2950 | ADP29656 | AAE25571 | ABP96442 | ADS11014 | ADQ67776 | ABB76931 | ABU52589 | ADS12237 | ADS12238 | ABB99355 | ADD3751   | <b>AEF1885</b>     | AAM38898 | ADN9512  | AAM40684 | AAE04910 |
| 20.0      |         | Ä       | AD      | ABI      | ADE     | ADI     | AD       | ¥        | ABI      | ADS      | Ā        | ABE      | ABI      | Ä        | ADS      | ABE      | Ā         | Ā                  | Æ        | AD       | AA       | AAI      |
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| 107       | 1 0     | 200     | 450     | 470      | 470     | 433     | 431      | 427      | 477      | 393      | 455      | 200      | 263      | 322      | 322      | 485      | 485       | 485                | 504      | 504      | 516      | 476      |
|           |         |         |         |          |         |         |          |          |          |          |          |          |          |          |          |          |           |                    |          |          |          |          |
| 0         |         | ر.<br>ت | 2.3     | 8.6      | 8.6     | 9.3     | 9.5      | 8.7      | 7.4      | 5.7      | 2.7      | 2.4      | 51.2     | 1.2      | 1.2      | 6.0      | 6.0       | 6.0                | 50.9     | 6.0      | 50.9     | 0.7      |
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| 1         |         | T244    | 1539    | 476.5    | 476.5   | 463     | 1461     | 448.5    | 1416.5   | 5.5      | 1301     | 3.5      | 1263     | 263      | 263      | 5.5      | 5.5       | 5.5                | 1255.5   | 5.5      | 5.5      | 2.5      |
| 1677      | 1       | _       | H       | 147      | 147     | Н       | 1        | 144      | 141      | 137      | -        | 129      | 1        | ٦        | -        | 125      | 125       | 1255               | 125      | 125      | 125      | 125      |
| Š         | 7 1     | 22      | 56      | 27       | 28      | 29      | 30       | 31       | 32       | 33       | 34       | 35       | 36       | 37       | 38       | 39       | 40        | 41                 | 42       | 43       | 44       | 45       |
|           |         |         |         |          |         |         |          |          |          |          |          |          |          |          |          |          |           |                    |          |          |          |          |

## ALIGNMENTS

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Beasley EM;
                                                                                                                                                                                                                                                                                                      New human transporter peptide, useful for preparing a composition for treating a disease or condition mediated by human transporters.
                                                                                                                                                                                                                                                           Di Francesco V,
                                                                                                                                                                                                                                                           Ketchum KA,
                                                                                       peptide therapy; human; transporter.
                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 2; 94pp; English.
                ADF90164 standard; protein; 476 AA
                                                                                                                                                          14-MAR-2001; 2001US-00805456.
                                                                                                                                                                             22-DEC-2000; 2000US-0257175P.
                                                                                                                                                                                                                                                          Merklov GV,
                                                   26-FEB-2004 (first entry)
                                                                     Human transporter protein.
                                                                                                                                                                                             (WEIM/) WEI M.
(YANC/) YAN C.
(WERK/) MERKLON G V.
(KETC/) KETCHUM K A.
(DERA/) DI FRANCESCO V.
(BEAS/) BEASLEY E M.
                                                                                                                                                                                                                                                                            WPI; 2003-898259/82.
N-PSDB; ADF90163.
                                                                                                                        US2003170778-A1.
                                                                                                                                                                                                                                                            Yan C,
                                                                                                        Homo sapiens.
                                                                                                                                          11-SEP-2003.
                                  ADF90164;
                                                                                                                                                                                                                                                            Wei M,
RESULT 1
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Query Match
Best Local Similarity 100.0%;
Matches 476; Conservative 0
        N-PSDB; ADR03798, ADR03800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
2004-552659/53
                                                                                                                                                                                 Sequence 476 AA;
                                           transporters,
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                                                          Claim 12;
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/note= "Encoded by CCCCCTC (SEQ ID 3 only)"
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by a human transporter protein. This human transporter protein.
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14-MAR-2001; 2001US-00805456.
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                          Sequence 476 AA;
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New nucleic acid encoding human transporter peptides, useful for preparing agents for treating a disease or condition mediated by human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2469; DB 8;
Pred. No. 7.4e-258;
0; Mismatches 0;
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                                                                                                                                          SEQ ID NO 2; 62pp; English
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cardiac disorder; angina; Alzheimer's disease; amnesia; epilepsy; schizophrenia; sickle cell anaemia; infertility; hyperglycaemia; sickle cell anaemia; infertility; hyperglycaemia; hypercholesterolaemia; stroke; multiple sclerosis; motor neuron disorder; prion disease; metabolic disease; developmental disorder; central nervous system; cardiomyopathy; hypertension; asthma; AIDS; allergy; anaemia; atherosclerosis; atopic dermatitis; diabetes mellitus; osteoarthritis; osteoporosis; rheumatoid arthritis; psoriasis; infection; trauma; hepatitis; cancer;
fibrosis; diabetes; Parkinson's disease; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukemia; lymphoma
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Homo sapiens.

WO2003016493-A2.

27-FEB-2003

16-AUG-2002; 2002WO-US026323

2001US-0313242P. 2001US-0324782P. 17-AUG-2001; 21-SEP-2001; 02-OCT-2001;

2001US-0328184P. 2001US-0345937P. 2001US-0335698P. 2001US-0332804P. 27-NOV-2001; 2001US-0333922P. 26-APR-2002; 2002US-0375637P. 01-NOV-2001; 13-NOV-2001; 26-OCT-2001;

(INCY-) INCYTE GENOMICS INC

11-JUN-2002; 03-MAY-2002;

2002US-0377444P 2002US-0388180P Tang YT, Lal PG, Yue H, Baughn MR, Nguyen DB, Yao MG, Greene BD; Borowsky ML, Lee S, Emerling BM, Xu Y, Becha SD, Gorvad AE; Azimzai Y, Yue H, Elliott VS, Lee EA, Yang J, Lehr-Mason PM; Ramkumar J, Lee SY, Faris M, Turner C, Furness M, Buchbinder JL; Walia NK, Li JX, Forsythe IJ, Griffin JA, Gietzen KJ, Swarnakar A; Hafalia AJA, Lindquist EA, Jiang X, Jackson AA, Wilson AD, Jin P; Khare R, Marquis JP;

WPI; 2003-268319/26.

N-PSDB; ABX12019.

Novel human transporter and ion channel polypeptides and polynucleotides for diagnosing, preventing or treating cell proliferative, transport, neurological, muscle and immunological disorders.

·Claim 1; Page 216-217; 253pp; English.

The invention discloses isolated polypeptides chosen from human transporter and ion channel polypeptides, TRICH 1-26, a biologically active or immunogenic fragment and the nucleic acids encoding them. Also disclosed are isolated antibodies raised against the TRICH proteins, methods for detecting a target polynuclectide in a sample and a microarray where at least one element is a TRICH polynuclectide. The proteins are useful for screening for agonists or antagonists, which can then be used for treating a disease or condition associated with corresponding for a compound that modulates the activity of the polypeptide or that binds to the polypeptide or as an immunogen for preparing or that binds to the polypeptides are useful for screening for compounds which alter expression of a target polynuclectide or for assessing to attibodies. The polyprotectides are useful for screening for compounds which alter expression of a target polynuclectide or for assessing toxicity of a test compound. The polypeptides, polynuclectides, contained and immunological disorders, such as amyotrophic lateral cherapy) and prevention of cell proliferative, transport, neurological, cancer, cardiac disorders, angina, Alzheimer's disease, prostate cancer, cardiac disorders, angina, Alzheimer's disease, amnesia, calcersis, cystic fibrosis, diabetes, parkinson's disease, metabolic disease of the central nervous system, developmental disorders of the central nervous system, cardiomyopathy, hypertension, asthma, Alds, allergies, anaemia, 

21-AUG-2001; 2001US-0313907P. 21-AUG-2002; 2002US-00225810.

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                                                                                                                                                                                                      IGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTV 120
                                                                                                                                                                                                                              IGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTV 151
                                                                                                                                                                                                                                                                                      211
                                                                                                                                                                                                                                                                                                                               ORIPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVT 331
                                                                                                                                                                                                                                                                                                                                                                                                                             ILYISLGCLGYLOFGANIQGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                              PFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLDLVISLVGSVSSSALALIIPPLLE 420
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            osteoporosis, rheumaloid arthritis, psoriasis, infections, trauma, hepatitis and cancers, including leukemia and lymphoma. The sequences presented in ABG75819-ABG75844 are the TRICH proteins of the invention
                                                                                                                                                                                                                                                                            152 MYGLESSPCSWLRNHAHWGRRVVDFFLLVTQLGFCCVYFVFLADNFKQVIEAANGTTNNC
                                                                                                                                                                                                                                                                                                                 HINNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIV
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                                                                                                                                                                 MYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTTNNC
atherosclerosis, atopic dermatitis, diabetes mellitus, osteoarthritis,
                                                                                                                                                  1 MSTQRLRNEDYHDYSSTDVSPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGN
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                                                                                                                      Gaps.
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                                                                                                                      Indels 0;
                                                                                            Length 507;
                                                                                           99.9%; Score 2466; DB 6;
99.8%; Pred. No. 1.7e-257;
ive 1; Mismatches 0;
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                                                                                                           3est Local Similarity 99.8
Aatches 475; Conservative
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                                                                   Sequence 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising a cDNA sequence encoding mouse tramdorin (tramd) 2, mouse tramd 3, human tramd 1, human tramd 2, human tramd 3 or rat tramd 1, or the genomic sequence of mouse tramd 1 or mouse tramd 3. Mouse tramd 1 is located to chromosome 11, whereas human tramd 1 is located to chromosome 5q31-33. The tramd sequences have neuroprotective, nootropic, analgesic and cerebroprotective activities, and can be used in gene therapy. The nucleic acid sequences are useful for diagnosing and treating central nervous system (CNS) disorders such as multiple sclerosis, nerve injury, neuropathic pain, stroke or trauma, and non-CNS disorders. The present "sequence represents human tramd 3, which is given in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                New nucleic acid sequence encoding tramdorins, e.g. mouse tramd 1, mouse tramd 3, human tramd 1, human tramd 2, human tramd 3 or rat tramd 1, useful for treating CNS, e.g. stroke, multiple sclerosis, trauma, neuropathic pain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes an isolated nucleic acid sequence
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Pred. No. 5.5e-257;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                Example 11; Fig 21; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.8%;
Matches 475; Conservative
(MCLA-) MCLAUGHLIN RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention
                                                                                                                        2003-278567/27.
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                                                                 Bermingham JR;
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Human; immunogen; NOVX; metabolic disorder; diabetes; cardiomyopathy;
                                   obesity; infectious disease; anorexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic disturbance; metabolic syndrome X; wasting disorder; cancer; gene therapy.
                                                                                                                                           2001US-0270523P.
2001US-0270797P.
2001US-0270810P.
2001US-0276400P.
2001US-027677P.
2001US-027677P.
2001US-028521P.
2001US-0281521P.
                                                                                                                                                                                                             2001US-0291765P.
2001US-0311595P.
2001US-0311980P.
2001US-0318526P.
2001US-0322712P.
                                                                                                                                                                                                                                                   2001US-0330307P
(first entry)
               Human NOVX protein, NOV7b.
                                                                                         WO200281518-A2.
                                                                           Homo sapiens.
                                                                                                                      21-FEB-2002;
                                                                                                                                     21-FEB-2001;
                                                                                                                                                                  08-MAR-2001;
                                                                                                                                                                          16-MAR-2001;
16-MAR-2001;
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04-APR-2001;
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04-MAR-2003
                                                                                                        17-OCT-2002
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Liu X; FL; New isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease Pena CEA, Shimkets RA, Li L, Shenoy SG, Kekuda R, Spytek KA; Vernet CAM, Malyankar UL, Guo X, Gusew VY, Casman SJ, Boldog Furtak K, Tchernev VP, Patturajan M, Sangolli EA, Padigaru M, Baumgartner JC, Gerlach VL, Spaderna SK, Zerhusen BD; WPI; 2003-046859/04. N-PSDB: ABX70643

(CURA-) CURAGEN CORP.

Claim 1; Page 57; 479pp; English. cancer.

and

Parkinson's disease, immune disorders, haematopoietic disorders, and various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases, various cancers, endocrine, connective tissue, blood, vascular, skin, renal, bone, brain, muscle disorders, or bacterial, fungal, protozoal or viral infections. NOVX, NOVX NA or ab is useful in screening

ABU52588 standard; protein; 496 AA

ABU52588;

ABUS2588
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assays, detection assays, predictive medicine, and in methods of treatment. NOVX is useful as immunogen, to screen for potential anti-degonist compounds, and as bait protein in a two-hybrid or three-hybrid assay. NOVX NA is useful in gene therapy, to express NOVX, to detect NOVX mRNA or a genetic lesion in a NOVX gene, and to modulate NOVX activity. The cell is useful for producing non-human transgenic animals. Ab is useful for isolating, and purifying NOVX and to monitor protein levels in tissue as part of a clinical testing procedure. The present sequence represents a NOVX protein
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                                                                                                                                                                                                                                                                                         IGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTV
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                                                                                                                                                                                                                                                                                                                             MYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTTNNC
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                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; transporter and ion channel; TRICH; transport disorder; neurological disorder; muscle disorder; immunological disorder; cell prolliferative disorder; neuroprotective; nootropic; cerebroprotective; immunosuppressive; cytostatic; respiratory;
                                                                                                                                                                                          ö
                                                                                                                                                                Length 496;
                                                                                                                                                                                        1; Indels
                                                                                                                                                              Score 2460; DB 6;
Pred. No. 7.4e-257;
); Mismatches 1;
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                                                                                                                                                              Query Match
Best Local Similarity 99.8%;
Matches 475; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of a number of human transporter and ion channel proteins, designated TRICH-1-TRICH-32. The sequences can be used in the treatment of transport, neurological, muscle, immunological and cell proliferative disorders. The present sequence is a protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosing,
immunological
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                                                                                                                                                                            L;
Yang ,
                                                                                                                                                                                                                                                                              Khan
                                                                                                                                                                      Raumann BE, Thornton M, Ding L, Yue H, Tang YT, Harland L;
Burford N, Greene BD, Sanjanwala MS, Baughn MR, Yao MG, Yang
Patterson C, Gandhi AR, Hafalia AJA, Tribouley CM, Walia NK;
Au-Young J, Walsh RT, Ramkumar J, Lu Y, Lu DAM, Azimzai Y,
Elliott VS, Nguyen DB, Xu Y, Seilhamer JJ, Borowsky ML, Khan
Kearney L, Thangavelu K, Das D, Policky JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2402.5; DB 5; Length 568;
Pred. No. 1.5e-250;
0; Mismatches 2; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                          New human transporters and ion channel polypeptides for treating or preventing transport, neurological; muscle, cell proliferative disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 155-156; 230pp; English
2000US-0216547P.
2000US-0218232P.
2000US-0220112P.
2000US-0221839P.
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88.3%;
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Matches 474; Conservative
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                                                                         28-JUL-2000;
                           14-JUL-2000;
21-JUL-2000;
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disorder in a subject, preferably human. Ab is useful for determining the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polypeptide termed NoVX (NOV1, 2a, 2b, 3a, 3b, 4a, 4b, 5, 6, 7a-c, 8a-e, 9a-b, 10, 11, 12a-c, 13, 14, 15, 16a-d, 17a-b, 18, 19, 20a-b, 21-30) appearing as ABU52578-ABU526549, a variant of NOVX, a mature form of NOVX, and a variant of the mature form of NOVX. Also included are a nucleic acid molecule (NOVX NA) encoding NOVX, or a fragment or complement of NOVX NA, a vector comprising NOVX NA, a cell comprising the vector, an anti-NOVX antibody (ab), determining the presence or amount of NOVX or NOVX NA in a sample, and identifying an agent that binds or modulares the expression or activity of NOVX. NOVX, NOVX NA or ab is useful for treating or preventing a NOVX-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FL;
Liu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
                                                                                                                 Human; immunogen; NOVX; metabolic disorder; diabetes; cardiomyopathy; obesity; infectious disease; anorexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic disturbance; metabolic syndrome X; wasting disorder; cancer; gene therapy; SNP;
                                                                                                                                                                                                                                                              /note= "May be Val as a result of a single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pena CEA, Shimkets RA, Li L, Shenoy SG, Kekuda R, Spytek KA; Vernet CAM, Malyankar UL, Guo X, Gusev VY, Casman SJ, Boldog Furtek K, Tchernev TY, Patturajan M, Gangolli EA, Padigaru M, Baumgartner JC, Gerlach VL, Spaderna SK, Zerhusen BD;
                                                                                                                                                                                                                                     Location/Qualifiers
                ABUS2587 standard; protein; 500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 56; 479pp; English
                                                                                                                                                                                     single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2001; 2001US-0270523P.
23-FEB-2001; 2001US-0270797P.
23-FEB-2001; 2001US-0270797P.
08-MAR-2001; 2001US-0276400P.
16-MAR-2001; 2001US-0276400P.
26-MAR-2001; 2001US-027677P.
26-MAR-2001; 2001US-0276677P.
25-APR-2001; 2001US-028654BP.
                                                                                                                                                                                                                                                                             polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-AUG-2001; 2001US-0311595P.
13-AUG-2001; 2001US-0311980P.
10-SEP-2001; 2001US-0318226P.
17-SEP-2001; 2001US-0322712P.
                                                                                                                                                                                                                                                                                                                                                       21-FEB-2002; 2002WO-US005374
                                                                  (first entry)
                                                                                           Human NOVX protein, NOV7a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-046859/04.
N-PSDB; ABX70642.
                                                                                                                                                                                                                                                  Misc-difference 173
                                                                                                                                                                                                                                                                                                    WO200281518-A2
                                                                                                                                                                                                               Homo sapiens
                                                                  04-MAR-2003
                                                                                                                                                                                                                                                                                                                               *17-0CT-2002
                                         ABU52587;
  ABU52587
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presence or amount of NOVX in a sample. NOVX is useful for identifying an agent that binds to NOVX. NOVX NO or ab is useful for identifying an agent that binds to NOVX. NOVX NO or ab is useful for treating concerned diabetes, cardiomyopathy, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, and various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic disease, various cancers, endocrine, connective tissue, blood, vascular, skin, renal, bone, brain, muscle disorders, or bacterial, fungal, protozoal or viral, infections. NoVX NA or ab is useful in screening assays, detection assays, predictive medicine, and in methods of treatment. NoVX is useful as immunogen, to screen for potential confoundation or three-or hybrid assay. NOVX NA is useful in gene therapy, to express NOVX, to detect NOVX mRNA or a genetic lesion in a NOVX gene, and to modulate NOVX activity. The cell is useful in gene therapy, to express NOVX, to activity. The cell is useful in gene therapy, to express NOVX, to activity. The cell is useful in gene therapy, to express NOVX activity. The cell is useful in gene therapy to express NOVX activity. The cell is useful in gene therapy to express NOVX activity. The cell is useful in NOVX and to monitor protein to be sequence represents a NOVX protein
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Pred. No. 3.9e-250;
0; Mismatches 0;
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97.5%;
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Best Local Similarity 97.5
Matches 472; Conservative
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ID ABB'
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AC ABB'
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DT 22-C
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DE HUMG
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Human VG51

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                          neurotransmitter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTTNNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                       used e.g. to screen for but low affinity transporter
                antihypertensive; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
             Antiasthmatic, anxiolytic; antiepileptic; antihypertensive; hu psychotropic; glutamate transporter; transporter; GABA; gamma-aminobutyric acid transporter; GABA transporter; GABA transporter; GABA transporter; asthma; anxiety; epilepsy; hypertension; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2324; DB 4;
Pred. No. 3.8e-242;
9; Mismatches 17;
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                                                                                                                                                                                                                                       & RECH MEDICALE
                                                                                                                                                                                                                                                                                                                                    New mammalian amino acid transporter, psychotropic agents, is high capacity gamma-aminobutyric acid.
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                                                                                                                                                                                2000WO-FR001383
                                                                                                                                                                                                            99FR-00006525
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94.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            450; Conservative
                                                                                                                                                                                                                                                                   Gasnier B,
                                                                                                                                                                                                                                                                                              WPI; 2001-025160/03.
                                                                    neurotic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                            N-PSDB; ABL57930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 476 AA;
                                                                                                                         WO200071709-A1.
                                                                                                                                                                                                                                       (INRM ) INSERM
                                                                                                                                                                                19-MAY-2000;
                                                                                               Homo sapiens
                                                                                                                                                                                                            21-MAY-1999;
                                                                                                                                                     30-NOV-2000.
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Best Local S
Matches 450
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The invention describes an isolated peptide comprising a 476 amino acid sequence (S1) or its allelic variant, orthologue or fragment, where the allelic variant to rothologue is encoded by a nucleic acid that hybridises under stringent conditions to the opposite strand of a nucleic acid comprising a sequence having 2093 or 46649 base pairs, and the fragment comprises 10 contiguous amino acids of S1. The peptide is useful for preparing a composition for treating a disease or condition mediated by a human transporter protein. This is the amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSTQRLRNEDYHDYSSTDVSPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Beasley
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human transporter peptide, useful for preparing a composition treating a disease or condition mediated by human transporters.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2324; DB 7;
Pred. No. 3.8e-242;
); Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                       Ketchum KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 7; 94pp; English.
                                                                                                                                                   7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human transporter protein homologue.
                                                                                                                                                                          human.
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                                                                                                                                                   seg id
                                                                               standard; protein; 476
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94.5%;
                                                                                                                                                                                                                                                                       14-MAR-2001; 2001US-00805456
                                                                                                                                                                                                                                                                                              22-DEC-2000; 2000US-0257175P
                                                                                                                                                                                                                                                                                                                                                                                                       Merklov GV,
                                                                                                                                                   Human transporter homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.5
Matches 450; Conservative
                                                                                                                                                                                                                                                                                                                     WEI M.
YAN C.
MERKLOV G V.
KETCHUM K A.
DI FRANCESCO V
                                                                                                                                                                                                                                                                                                                                                                                BEASLEY E M.
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-898259/82.
                                                                                                                           (first
                                                                                                                                                                          peptide therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 476 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                       Yan C,
                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                           FFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLDLVISLVGSVSSSALALIIPPLLE 420
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HINDETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIXQFIV
                                                                                                                                                                             361 VIVSWVCKCCTLMVDLGIGSAMLCKTCILAILIPRLDLVISLVGSVSSSALALIIPPFLLE
                                                                                                   ILYISLGCLGYLQFGANIQGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIP
                                          QRIPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVT
                                                                                                                                                                                                                   VITEYSEGMSPLTIFKDALISILGFVGFVVGTYEALYELIQPSNAPIFINSTCAFI 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding human transporter peptides, useful for preparing agents for treating a disease or condition mediated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beasley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2324; DB 8;
Pred. No. 3.8e-242;
9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                            novel transporter protein.
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14-MAR-2001; 2001US-00805456.
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                                                                                                                                                                                                                                                                                                                                                                                                          Human homologue of
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; transporter
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New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika
Otsuka M, Nagahari K, Masuho Y;
                                    361 VIVSWVCKCCTLMVDLGIGSAMLCKTCILAILIPRLDLVISLVGSVSSSALALIIPPLLE
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MSTQRLRNEDYHDYSSTDVSPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGN
                                                                                          MYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTTNNC
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RES ASSOC BIOTECHNOLOGY.
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24-JAN-2002; 2002US-0350435P
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Seki N, Yoshikawa T,
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N-PSDB; ADA53869.
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(REAS-)
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Length 476; Indels σ

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                                                                                                                                                                                                                                                                                       Gaps
                              membrane
                     The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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                                                                                                                                                                                                                                                                                       42;
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                                                                                                                                                                                                                             Score 2217; DB 6;
Pred. No. 1.3e-230;
1; Mismatches 1;
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432; Conser
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                                                                                                                                                                                 Sequence 434
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The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haemacopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic protein of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
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                                                                                                                                                                                                                                                                                                                                                                                                MYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTTNNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HNNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIV
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Zhou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide, useful in preparing a composition for diagnos treating inflammatory, neurodegenerative or stem cell disorders, aplastic anemia or cancer for promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                     42;
Ö
 Weng
                                                                                                                                                                                                                                                                                                                        Length 434;
                                                                                                                                                                                                                                                                                                                                                    Indels
Xue AJ,
                                                                                                                                                                                                                                                                                                                      Score 2217; DB 8;
Pred. No. 1.3e-230;
1; Mismatches 1;
Σ̈́
Ghosh
                                                                                                                   SEQ ID NO 1252; 718pp; English.
 <sup>رر</sup>
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 Wang
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                                                                                                                                                                                                                                                                                                                           89.8%;
90.8%;
ø,
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Matches 432; Conservative
Zhao
Chen R,
                                                                                                                                                                                                                                                                                                 Sequence 434 AA;
                                      N-PSDB; ADS10331
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                                                                                                                   Claim 20;
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119
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360 AIVSRVPERFELVVDLSARTAMVCVTCVLAVLIPRLDLVISLVGSVSSALALIIPPLLE 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated nucleic acid sequence comprising a cDNA sequence encoding mouse tramdorin (tramd) 2, mouse tramd 3, human tramd 1, human tramd 2, human tramd 3 or rat tramd 1, or the genomic sequence of mouse tramd 1 or mouse tramd 3. Mouse tramd 1, or located to chromosome 11, whereas human tramd 1 is located to chromosome 5q31-33. The tramd sequences have neuroprotective, nootropic, analgesic and cerebroprotective activities, and can be used in gene therapy. The nucleic acid sequences are useful for diagnosing and treating central nervous system (CNS) disorders such as multiple sclerosis, nerve injury, neuropathic pain, stroke or trauma, and non-CNS disorders. The present sequence represents mouse tramd 3, which is given in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid sequence encoding tramdorins, e.g. mouse tramd 1, mouse and 2, mouse tramd 3, human tramd 1, human tramd 2, human tramd 3 or tramd 1, useful for treating CNS, e.g. stroke, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                      Neuroprotective; nootropic; cerebroprotective; analgesic; gene therapy; central nervous system disorder; CNS disorder; multiple sclerosis; nerve injury; neuropathic pain; stroke; trauma; non-CNS disorder; tramd; tramdorin; mouse; tramdorin 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSTQRLRNEDYHDYSSTDVSPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGN
                                     1;
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86.1%; Pred. No. 1e-222;
iive 32; Mismatches 3
                                                                                                                                                                                                                                                                                                     Mouse tramdorin 3 protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 11; Fig 23A; 177pp; English
                                                                                                                                                                                   Ą.
                                                                                                                                                                                   ABP96443 standard; protein; 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-2001; 2001US-0313907P.
21-AUG-2002; 2002US-00225810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-AUG-2002; 2002WO-US026637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MCLA-) MCLAUGHLIN RES INST.
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuropathic pain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention
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N-PSDB; ABZ80238.
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es 410; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003016502-A2
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                                                                                                                                                                                                                                                                  02-JUN-2003
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                                                                                                                                                                                                                        ABP96443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated nucleic acid sequence comprising a cDNA sequence encoding mouse tramdorin (tramd) 2, mouse tramd 3, human tramd 1, human tramd 3. Mouse tramd 1, contend 2, human tramd 3. Mouse tramd 1, or the genomic sequence of mouse tramd 1 or mouse tramd 3. Mouse tramd 1 is located to chromosome 5q31-33. The tramd sequences have neuroprotective, nootropic, analgesic and cerebroprotective activities, and can be used in gene therapy. The neuropathic gatemate are useful for diagnosing and treating central nervous system (CNS) disorders such as multiple sclerosis, nerve injury, neuropathic pain, stroke or trauma, and non-CNS disorders. The present sequence represents rat LYAAT-1, which is given in the exemplification of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLYISLGSLGYLQFGADIKGSITLNLPPNCWLYQSVKLLYSIGIFFTYALQFYVAAEIIIP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTTNNC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRIPDPSHLPLVAPWKTYPLFFGTA1FSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid sequence encoding tramdorins, e.g. mouse tramd 1, mous nd 2, mouse tramd 3, human tramd 1, human tramd 2, human tramd 3 or tramd 1, useful for treating CNS, e.g. stroke, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSTQRLRNEDYHDYSSTDVSPESPSEGLGSF-SPGSYQRLGENSSMTWFQTLIHLLKGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYGLECSPSTWIRNHSHWGRRIVDFFLVVTQLGFCCVYFVFLADNFKQVIEAANGTTTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HNNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSTQRLRNEDYHDYSSTDVSPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
      disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Indels
    non-CNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.9%; Score 2146.5; DB 6; 85.7%; Pred. No. 6.3e-223;
neuropathic pain; stroke; trauma;; LYAAT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 24; 177pp; English.
                                                                                                                                                                                                                          2001US-0313907P.
2002US-00225810.
                                                                                                                                                                                   21-AUG-2002; 2002WO-US026637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trauma, neuropathic pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-278567/27
                                                                                                                                                                                                                                                                                      (MCLA-) MCLAUGHLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABZ80241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 475 AA;
      injury; ne
rin; rat;
                                                                                                      WO2003016502-A2
                                                                                                                                                                                                                                                                                                                              Bermingham JR;
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                                                                                                                                                                                                                                               21-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408;
                        tramdorin;
                                                                Rattus sp.
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                                                                                                                                            1
                                                                                                Length 475;
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                                                                                                DB 4;
                                                                                                                                            31;
                                                                                           86.8%; Score 2142.5; DB 4
85.5%; Pred. No. 1.7e-222;
ive 37; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      completed: August 24, 2006, 01:19:44
                                                                                                                     Local Similarity 85.5
les 407; Conservative
                                              Sequence 475 AA;
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                                                                                                                     240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurotransmitter;
                                                                                                                                               QRIPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVT
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                                                                   MYGLECSPSTWVRNHSHWGRRIVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTTINC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   psychotropic; glutamate transporter; transporter; GABA;
gamma-aminobutyric acid transporter; GABA transporter; neurotr
asthma; anxiety; epilepsy; hypertension; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB76935 standard; protein; 475 AA
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N-PSDB; ABL57913.
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

August 24, 2006, 01:19:59; Search time 41 Seconds (without alignments) 1117.053 Million cell updates/sec

US-10-679-362-2 2469 1 MSTQRLRNEDYHDYSSTDVS..........YELIQPSNAPIFINSTCAFI 476

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: \* 2: pir2: \* 3: pir3: \* 4: pir4: \* PIR 80:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |        | de    |                       |    | SUMMARIES |                    |  |
|---------------|--------|-------|-----------------------|----|-----------|--------------------|--|
| Result<br>No. | Score  | Query | Query<br>Match Length | DB | ID        | Description        |  |
| 1             | 1677.5 | 67.9  | 481                   | 8  | JC7961    | proton-coupled ami |  |
| 7             | 672    | 27.2  | 607                   | ~  | T26845    | hypothetical prote |  |
| m             | 652    | 26.4  | 449                   | 7  | H88022    | protein T27A1.5 [i |  |
| 4.            | 465.5  | 18.9  | 436                   | ~  | T05653    | amino acid transpo |  |
| Ŋ             | 465.5  | 18.9  | 713                   | ~  | S58251    | probable membrane  |  |
| 9             | 464    | 18.8  | 434                   | ~  | T15799    | hypothetical prote |  |
| 7             | 462.5  | 18.7  | 481                   | N  | T23131    |                    |  |
| ۵             | 443.5  | 18.0  |                       | ~  | F88544    | protein F59B2.2 [i |  |
| σ             | 431.5  | 17.5  |                       | ~  | T26705    | hypothetical prote |  |
| 10            | 415    | 16.8  |                       | ~  | T38741    |                    |  |
| 11            | 388.5  | 15.7  |                       | ~  | 837976    | hypothetical prote |  |
| 12            | 368    | 14.9  | 389                   | ~  | S31123    |                    |  |
| 13            | 285.5  | 11.6  | 543                   | ~  | T48239    |                    |  |
| 14            | 276    | 11.2  | 516                   | ~  | T48238    | _                  |  |
| 15            | 274.5  | 11.1  | 426                   | ~  | T51506    | Н                  |  |
| 16            | 270.5  | 11.0  | 529                   | ~  | E84813    | _                  |  |
| 17            | 263    | 10.7  | 503                   | ~  | T26524    | _                  |  |
| 18            | 259    | 10.5  | 890                   | ~  | T21000    | _                  |  |
| 19            | 251.5  | 10.2  | 462                   | 7  | S42372    | hypothetical prote |  |
| 20            | 251.5  | 10.2  | 486                   | ~  | T42254    | amino acid permeas |  |
| 21            | 247    | 10.0  | 423                   | ~  | T49959    |                    |  |
| 22            | 233.5  | 9.5   | 571                   | 0  | T06737    | hypothetical prote |  |
| 23            | 233    | 9.4   | 484                   | ~  | T34016    | cal                |  |
| 24            | 232    | 9.4   |                       | ~  | S45413    | probable membrane  |  |
| 25            | 230    | 9.3   |                       | ~  | T16658    | cal pi             |  |
| 26            | 224    | 9.1   |                       | N  | C96505    | probable amino aci |  |
| 27            | 222    | 9.0   |                       | 7  | 820       | protein F21D12.3 [ |  |
| 28            | 215.5  | 8.7   |                       | ~  | 4818      | 2                  |  |
| 29            | Н      | 8.5   |                       | ~  | S50622    | hypothetical prote |  |

| hypothetical prote | probable lysine an | hypothetical prote | probable amino aci | probable transmemb | hypothetical prote | probable amino aci | protein F21J9.6 [i | hypothetical prote | amino acid permeas | hypothetical prote | amino acid transpo | amino acid transpo | amino acid transpo | probable membrane | amino acid permeas |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| 196738             | 86385              | S50525             | T00620             | T39523             | A96837             | H96802             | C86378             | T47737             | T50691             | S55188             | S52421             | JC7328             | T10100             | S49792            | T15052             |
| Ή                  | بتر                |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                   |                    |
| 2<br>E             | 2                  | ~                  | ~                  | N                  | 7                  | ~                  | ~                  | N                  | N                  | N                  | ~                  | N                  | ~                  | ~                 | ~                  |
| 2                  | 440 2 F            | 480 2              | 475 2              | 420 2              | 489 2              | 476 2              | 441 2              | 435 2              | 481 2              | 602 2              | 493 2              | 487 2              | 486 2              | 490 2             | 462 2              |
| 2                  | 8.1 440 2 F        | •                  | •                  | •                  | •                  | •                  | •                  | •                  | •                  | 7.3 602 2          | •                  | •                  | •                  | •                 | •                  |
| 2                  | 8.1                | 8.1                | •                  | 8.0                | •                  | 7.7                | 7.6                | 7.5                | 7.4                |                    | 7.3                | 7.0                | 7.0                | 6.9               | 6.7                |

## ALIGNMENTS

| <br>RESULT 1 JC7961 proton-coupled amino of Species: Rattus norr; Date: 25-Aug-2003 #F. Chen, Z.; Kennedy, Blochem, Blophys. Res A; Title: Structure, t. A; Reference number: JC7961 A; Molecule type: mRNA A; Residues: 1-481 cCH A; Res | RESULT 1 JC7961  JC7961  JC7961  Directon-coupled amino acid transporter 2 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 15-Sep-2003 C;Accession: JC7961 C;Accession: JC7961 C;Accession: JC7961 Biochem. Biophys. Res. Commun. 304, 747-754, 2003 A;Title: Structure, tissue expression pattern, and function of the amino acid transporte A;Reference number: JC7961; PMID:12727219 A;Reference number: JC7961; PMID:12727219 A;Reference number: JC7961 A;Residues: 1-481 cCHE> A;Reference number: JC7961 A;Residues: 1-481 cCHE> C;Comment: This transport protein is a second member of H+-coupled, pH-dependent, Na+-in sport not only from one cellular compartment to another (across plasma membranes) but all cG-Genetics: C;Genetics: A;Gene: pat2 A;Gene: pat2 A;Gene: pat2 A;Gene: pat2 A;Gene: pat2 A;Gene: pat2 |
|--|---|
| Query Mato<br>Best Local<br>Matches  | Query Match 67.9%; Score 1677.5; DB 2; Length 481; Best Local Similarity 71.7%; Pred. No. 2.7e-127; Matches 325; Conservative 54; Mismatches 67; Indels 7; Gaps 1;  |
| oy da  | 20 SPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGNIGTGLLGLPLAVKNAGIVM 79   : :     : :     : :  |
| ò qa   | 80 GPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDXGDTVMYGLESSPCSWLRNHAHWG 139<br>  :   :: ::  |
| <br>Oy 14  | 140 RRVVDFFLIVTQLGFCCVYFVFLADNFKQVIBAANGTINNCHNNETVILTPTMDSRLYML 199<br>  |
| <br>Oy 20  | 200 SFLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIVQRIPDPSHLPLVAPWKTYP 259<br>  |
| <br>Oy 26<br>Db 26   | 260 LFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVTILYISLGCLGYLOFGANIQ 319<br>  |
| <br>Oy 33  | 320 GSITLNLPNCWLYQSVKLLYSIGIFFTYALGFYVPAEIIIPFFVSRAPEHCELVVDLFVR 379<br>  |
| <br>δy . 3ε<br>Db .36  | 380 TVLVCLTCILAILIPRLDLVISLVGSVSSSALALIIPPLLEVTTFYSEGMSPLTIFKDAL 439<br>   :  :  :  |

and

Length 449;

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A;Molecule type: DNA
A;Residuss: 1-449 <STO>
A;Cross-treferences: UNIPROT:017275; UNIPARC:UP100000747F8; GB:chr_II; PIDN:AB71045.1; PII
C;Genetics:
A;Gene: T27A1.5
35, 1999; Science 283, 2103, 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                         87 IGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTVMYGLESSPCSWLRNHAHWGRRVVDFF 146
                                                                                                                                                                                                                                                                                                                                       19 GSHQPTWGEMFASRVRDSRSITADQALIHMIKVMMGTGMLSLPLAFKHSGIWLGLILLCF
                                                                                                                                                                                                                                                                                                                 36 GSYQ------RFGQSNSTTWFQTLIHLLKGNIGTGLLGLPLAVKNAGIVMGPISLLI
                                                                                                                                                                   A;Map position: 2
C;Superfamily: Arabidopsis amino acid transport protein I
                                                                                                                                                                                                                              26.4%; Score 652; DB 2; L ilarity 33.0%; Pred. No. 7.8e-45; Conservative 101; Mismatches 160;
published errata appeared in Science 283,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 LISILGFVGFVVGTYEALYELIQ 461
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es 146; Conserv
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                     A;Accession: H88022
A;Status: preliminary
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Matches 143;
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A;Introns: 53/3; 80/3; 110/2; 141/2; 169/3; 229/1; 261/3; 300/2; 320/2; 355/3; 377/1; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: H88022
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-607 <WIL>
A;Residues: 1-607 <WIL>
A;Cross-references: UNIPROT:045936; UNIPARC:UPI000017BC76; EMBL:AL021481; PIDN:CAA16336.
A;Experimental source: clone Y43F4B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLPLAFKHSGLFLGLILTVLICLICLYCMRQVVFAAHFVCNRNGRDLIDYANIMRGAVEM 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 SVTGFYGYLSLGNDVKDTATLNLPMTPFYQTIKLMFVACIMISYPLQFYVPMERIEKWIT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRAPEHCELVVDLFVRTVLVCLTCILALLIPRLDLVISLVGSVSSSALALIIPPLLEVTT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 GLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTVMYGLES 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTTNNCHNNETV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 ILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIVQRIPDP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I---HLSKAVWMLLLLIPMLSICSIRRLSILAPFAMAANVVYVVAVAVVLFFFLSDLRPI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKFPL---ILYLGMVIVTILY 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 ISLGCLGYLQFGANIQGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIPFFV 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YQEFDNEPEAPGDTEVQTPRRNTVSEDTSLFQDRLPTENSLTPEQAFIHMVKAMLGTGLL 68
                                                                                                                                                               hypothetical protein Y43F4B.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26845
R;Matchews, L.
submitted to the EMBL Data Library, January 1998
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSSTDVSPE-----ESPSEGLNNLSSPGS--YQRFGQSNSTTWFQTLIHLLKGNIGTGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95; Mismatches 180; Indels
                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, January 1998
A;Reference number: 220276
A;Accession: T26845
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                     440 ISILGFVGFVVGTYEALYELIQPSNAPIFINST 472
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                                             Best Local Similarity 33.3
Matches 150; Conservative
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                                                                                                                     262
                                                                                                                                                           240 GTVWFAFEGVAVVLPIENQMNEPIHFITPNGVLNTSCILVLLVYMTVGFFGFLRYGNDIK 299
                                                                                                                                                                                                                                                                                                                                                                  320 GSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIPFFVSRAPEHCELVVDLFVR 379
147 LIVTQLGFCCVYFVFLADNFKQVIEAANGTTNNCHNNE----TVILTPTMDSRLYMLSFL 202
                                                               .---- 181
                                                                                                                                                                                                                                             GTAIFSFEGIGMVLPLENKMKDPRKFPL---ILYLGMVIVTILYISLGCLGYLQFGANIQ 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 TVLVCLTCILAILIPRLDLVISLVGSVSSALALIIPPLLEVTTFYS-EGMSPLTIFKDA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid transport protein homolog F22113.20 - Arabidopsis thaliana C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 FQTLIHLLKGNIGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRL |:| :: :: || :|| | | | | | : | :: :: || :|| :| | : ||
                                                                                                                     203 PFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIVQRIPDPSHLPLVAPWKTYPLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-438 <BEV.
A;Residues: 1-438 <BEV.
A;Cross-references: UNIPROT:Q9SVGO; UNIPARC:UPI00000A7D30; EMBL:AL035539
A;Experimental source: cultivar Columbia; BAC clone F22113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 436;
                                                            MFVAQFGFCCVYFVFMADNLKQFFD----QTSSIHISQAGWIALLLIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 4
A;Note: F22113.20
C;Superfamily: Arabidopsis amino acid transport protein I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.9%; Score 465.5; DB 2;
llarity 32.4%; Pred. No. 7.6e-30;
Conservative 66; Mismatches 155;
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A,Cross-references: UNIPROT:Q18595; UNIPARC:UPI000017B834; EMBL:U28928; NID:g861301; PID A,Experimental source: strain Bristol N2 C,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLGFCCVYFVFLADNFKQVIEAANGTTNNCHNNETVILTPTMDSRLYMLSFLPFLVL-LV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C44B7.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 VILINLPQSNIFVNLIQLFYSIAIMLSTPLQLFPAIKIIENKFFPKFTKIYVKHDDLTTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSRPDHMKVLPSAKGTTSTKKVFLILLKSFIGTGVLFLPNAFHNGGLFFSVSMLAFFGIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 FIRNLRALSIFSLLANITMLVSLVMIYQFIVQRI-PDPSHLPLVA------PWKTYPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .374 VDL-------FVRTVLVCLTCILAIL-IPRLDLVISLVGSVSSSALALIIP
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                                                                                                                                                                                                                                      73;
                                                                                                                                                                                    713;
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                                                                                                                                                                                      Length
                                                                                                                                                                                                                                         Indels
                   predicted fm6>
predicted fm7>
predicted fm7>
predicted fm8>
predicted fm9>
predicted fm9>
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submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid C44B7.
A;Reference number: S61146
A;Accession: T15799
A;Accession: T15799
A;Molecule type: DNA
A;Residues: 1-434 < DUZ>
                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                          ; Pred. No. 1.3e-29;
81; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1e-29;
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                                                                                                                                                                                      18.9%; Score 465.5; 31.0%; Pred. No. 1.3
F;486-502/Domain: transmembrane #status F;516-532/Domain: transmembrane #status F;557-573/Domain: transmembrane #status F;626-642/Domain: transmembrane #status F;649-665/Domain: transmembrane #status F;689-705/Domain: transmembrane #status F;
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Matches 125; Conservative
                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                            144;
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                                                                                                                                                                                                                                                                                                                                            임
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N;Alternate names: hypothetical protein N2185
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: SS8251; S63041; S63953
K;Saiz, J.E.; Bultrago, M.J.; Soler, A.; del Rey, F.; Revuelta, J.L.
submitted to the EMBL Data Library, July 1995
A;Pescription: The sequence of a 21.3 Kb fragment from the left arm of yeast chromosome A;Reference number: S58246
A;Reference number: S58246
A;Reference number: S58246
A;Residues: 1-713 <SAI>A;Residues: 1-713 <SAI>A;Reference number: S63037
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A;Ratus: nucleic acid sequence not shown
A;Ratus: nucleic acid sequence not shown
A;Ratus: nucleic acid sequence
A;Ratus: nucleic acid sequence
A;Ratus: NasAP-
A;Cross-references: UNIPARC:UPI0000052E6D; EMBL:Z50161; NID:g929846; PIDN:CAA90525.1; I
C;Genetics:
A;Cross-references: SGD:S0005045
A;Cross-references: SGD:S0005045
A;Nap position: 14L
A;Note: YNL101w
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YNL101w
C;Reywords: transmembrane protein
F;302-318/Domain: transmembrane #status predicted <TML>
F;310-426/Domain: transmembrane #status predicted <TML>
F;442-458/Domain: transmembrane #status predicted <TML>
F;442-458/Domain: transmembrane #status predicted <TML>
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                                                                                          92 LDSFNAGISKIGSFGD-----LGFAVCGSL-----GRIVVDLFILLSQAGFCVGYLIFI 140
                                                                                                                                                                --MDSRLYMLSFLPFL 205
                                                                                                                                                                                                                                                                                                                                                                                   ---FGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVTILYISLGCLGYLQFGANI 318
                                                                                                                                                                                                                                                                                                                                                                                                                  QGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPABIIIPFFVSRAPEHCELVVDLFV 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTVLVCLTCILAILIPRLDLVISLVGSVSSSALALIIPPLLEVTTFYSEGMSPLTIFKDA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 RWYLVLAVTLVÅLFVPNFADFLSLVGSSTCCVLGFVLPALFHLLVF-KEEMGWLQWSSDT 410
                                                           NKSF-----VDYGDTVMYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFL 162
                                                                                                                                                                                                                     -----GTTLANLSDPE----SPTSLRHQFTRLGSEFLGVSSKSLYIWGCFPFQ 184
                                                                                                                                                                                                                                                                           206 VLLVFIRNLRALSIFSLLANI----TMLVSLVMIYQFIVQRIPDPSHLPLVAPWKTYPLF 261
     37 FKTFANVFIAVVGAGVLGLPYAFKRTGWLMGVLLLVSVSVLTHHCMMLLV----YTRRK 91
                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UP10000052E6D; EMBL:Z71377; NID:g1302013; PIC A;Experimental source: strain S288C
R;Saiz, J.E.; Buitrago, M.J.; Soler-Mira, A.; del Rey, F.; Revuelta, J.L. Yeast 12, 403-409, 1996
                                                                                                                                                                ADNFKQVIEAANGTT-NNCHNNETVILTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439 LISILGFVGFVVGTYEALYEL 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 AIVVLGVVLAVSGTWSSLSEI 431
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A; Molecule type: DNA
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C)Accession: F88544

R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology, A;Title: Genome sequence of the nematode C. elegans; a platform for investigating biology, A;Note: see websites genome wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Cross-references: UNIPROT: P34479; UNIPARC: UP1000013B9DA; GB: chr_III; PIDN: CAA77582.1; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 VTILYISLGCLGYLQFGANIQGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEII 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 I----PFFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLDLVISLVGSVSSSALALI 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 NNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIVQ 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 RIPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKF--PL-ILYLGMVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSPCSWLRNHAHWGRRVVDFFLIVT----QLGFCCVYFVFLADNFKQVIEAANGTINNCH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T26705

hypothetical protein Y38H6C.17 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 PSLPYAWKLGGLWVSFVMSFVIAGLNWYGNHILVRASQHLAKKSDRSALDYGHFAKKVCD
                                                                                                                                                                                                                                                                                                                                  C.Species: Caenorhabditis elegans
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                            --DALISILGFVGFVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LRNEDYHDYSSTDVSPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGNIGTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415 IPPLLEVITEYSEGMSPLT-----IFKDALISILGFVGFVVGTYEALYELIQPSNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
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                                                                                                                                                                                                                                                                                                        protein F59B2.2 [imported] - Caenorhabditis elegans
  VSSSALALIIPPLLEVTTFYSEGMSPLTIFK-
                                                                                                                                               | :: :: |
469 LYSSIDDII 477
                                                                                                             452 TYEALYELI 460
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A;Residues: 1~460 <STO>
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  406
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A;Experimental source: clone H32K16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                        LOFYVPAEIIIPFFVSRAPEHC-----ELVVDLFVRTVLVCLTCILAILIPRLDLVISL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVDYGDTVMYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VMIYQFIVQRIPDPS-HLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKF--- 288
                                                                                                                                                                                                                                                                                                                                                                 FGVLSVGVGMVVVIYSFAGFFGFLTYGNDVQDSITLNLPNDHLGIFVKAVLLFVVYSGFL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apportetical protein H32K16.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Sacession: T23131
R;Wallis, J
R;Wallis, J
R;Wallis, J
R;Wallis, J
R;Reference number: Z19691
A;Reference 
                                                                                                                                                                                                -VMIYQFIVQRIPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPR--KFP
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                                                                                   ANGTINNCHNNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITMLVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGSVSSSALALIIPPLLEVTTFYSEGMSPLTIFKDALISILGFVGFVVGTYEALY 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: CESP:H32K16.1
A,Map posttion: 1
A;Introns: 64/2; 94/3; 124/2; 155/2; 183/3; 240/3; 337/2; 397/1; 444/2
C,Superfamily: Arabidopsis amino acid transport protein I
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                                                                                                                                          ---VMNDVPSRAT--LFPMV----
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R;White, S.

Submitted to the EMBL Data Library, September 1998
A;Reference number: Z20255
A;Accession: T26705
A;Accession: T26705
A;Accession: T26705
A;Accession: U26705
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: DNA
A;Residues: 1-467 < WLL>
A;Residues: 1-467 < WLL>
A;Residues: L-467 < WLL>
A;Resid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 ALITQELLSHTWYPTWELPSITGVEGVSLAAGSLİYSFEGQAMVLPLENSLKHPQDMRGL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIHLLKGNIGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                           17.5%; Score 431.5; DB 326.8%; Pred. No. 4.4e-27
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Matches 116; Conservative
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RESULT 10
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A,Title: DNA sequencing of a 36.2 kb fragment located between the FAS1 A,Reference number: S44563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: strain S288C
R;Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle,
Yeast 10, 35-40, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-132 <VA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S44582
major facilitator protein homolog - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-199 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38741
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, December 1995
A;Reference number: 221808
A;Reference number: 221808
A;Accession: T38741
A;Status: prellminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-656 cGEN>
A;Reperimental source: strain 972h-; cosmid c3H1
C;Genetics: A;Rap posttion: 1
A;Introns: 299/2; 361/3; 593/2
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YNL101w
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PIDN: CAA81508.1;

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LAP4 loci

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D.; Hilger,

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A;Molecule type: DNA
A;Residues: 1-692 «VAN»
A;Cross-references: UNIPROT:F36062; UNIFARC:UPI000013B735; EMBL:Z28146; NID:g486250; PID
R;Ramezani Rad, M.; Xu, G.; Kirchrath, L.; Fritz, C.; Keuchel, H.; Hollenberg, C.P.
submitted to the Protein Sequence Database, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAP4
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                                                       12;
                                                                                                                                                            DEDIDDFAMPRDVNPSLIHSTVPSEQEPLISRHGRYKLQTPGNASNGKAVLL-LLKSFVG 290
                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                                                                 GLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTTNNCHN 182
                                                                                                                                                                                                                                                                                                                                                                                        381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --VISTTHREYHLAVFIFIQFLVPVPLSLVRKISKLSATALIADVFILLGILYLYFWDV 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRIPDPSHLPLVAPWKT-YPLFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TILYISLGCLGYLQFGANIQGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIII 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499 SLLFISIGLLSYAAFGSKVKTVVILNMPESTFTVIIQFLYAIAILLSTPLQLFPAIAIIE 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 PFFVSRAPEHCELVVDLFVRTVLVCLTCILAILI-----PRLDLVISLVGSVSSSALALI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559 QGIFTRSGKRNRKI---KWRKNYLRVLIVILAILISWAGSSRLDLFVSMVGSVCCIPLIYM 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the FAS1
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                                                                                                                                                                                                                                                                          291 TGVLFLPKAFKLGGLVFSSATLLIVGVLSHICFLLLIQTR----MKVPGSFGDIGGT-LY
                                                                                                                                                                                                                                                                                                                                                                                                                                            183 NETVILIPTMDSRLYMLSFLPFLVL--LVFIRNLRALSIFSLLANITMLVSLVMIYQFIV
                                                                                                        8 NEDYHDYS-STDVSP----EESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGNIG
                                                                                                                                                                                                                      TGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTVMY
                                                       Gaps
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A;Residues: 447-692 <RAM>
A;Cross-references: UNIPARC:UPI0000178F95; EMBL:Z28146; MIPS:YKL146w
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R; Vandenbol, M.; Bolle, P.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, September 1993
A, Description: DNA sequencing of a 36.2 kb fragment located between
A; Reference number: S37786
A; Accession: S37805
                                                         48;
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                                                                                                                                                                                                                                                                                                                                                                    C;Species: Saccharonyces cervisiae
C;Date: 03-May-1994 #text_change
C;Date: 03-May-1994 #text_change
C;Accession: S37976; S37975; S37805; S44582
C;Accession: S37976; S37975; S37805; S44582
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37976
A;Accession: S37976
Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cerevisiae)
Score 415; DB 2;
Pred. No. 1.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein YKL146w - yeast (Saccharomyces
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein YKL600
                                                 84;
  16.8%;
                            29.48;
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C;Species: Saccharomyces cerevis
C;Date: 03-May-1994 #sequence re
                                                         Conservative
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A;Accession: S37975
                               Similarity
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                            Best Local Sim
Matches 125;
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A;Status: preliminary A;Molecule type: DNA
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hypothetical protein F59B2.2 - Caenorhabditis elegans

hypothetical protein F59B2.2 - Caenorhabditis elegans

hypothetical protein F59B2.2 - Caenorhabditis elegans

C; Species Caenorhabditis elegans

C; Date: 20 Feb-1995 #sequence_revision 20 Feb-1995 #text_change 09-Jul-2004

C; Accession: Siliza

R; Sulston, J; Du, Z; Thomas, K; Wilson, R.; Hillier, L.; Staden, R.; Halloran, N.; Gx

awkins, T.; Ainscough, R.; Waterston, R.; Hillier, L.; Staden, R.; Halloran, N.; Gx

awkins, T.; Ainscough, R.; Waterston, November 1991

A; Description: The C. elegans sequencing project: A beginning.

A; Reference number: Siliza

A; Accession: Siliza

A; Affatus: preliminary

A; Molecule type: DNA
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-132 < VA3>
A;Residues: 1-132 < VA3>
A;Residues: 1-132 < VA3>
A;Residues: 1-132 < VA3>
A;Experimental source: strain $288C
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1993
C;Genetics:
A;Cross-references: SGD:S0001629
A;Map position: 11L
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YNL101w
C;Keywords: transmembrane protein
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A;Cross-references: UNIPROT:P34479; UNIPARC:UPI000017BA50; EMBL:Z11505; NID:g6718;
C;Genetics: 38/2; 59/2; 148/2; 343/3
A;Introns: 38/2; 59/2; 148/2; 343/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KM------KFAILSSIALSQIGFSAAYTVFTATNLQVFSE-----NFFH--- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466 AVNGVASDITMLMFNKADWS---LFIGTALFTFEGIGLLIPIQESMKHPKHFRPSLSAVMC 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVTILYISLGCLGYLQFGANIQGSITLNLPNCWLYQ-SVKLLYSIGIFFTYALQFYVPAE 356
                                                                                                                                                                                                                                                                                                                                                 SEBEBEBEBEBEBEBEBALETESTOLVSREHGRHPHKSSTV--KAVLLLLKSFVGTGVLF 317
                                                                                                                                                                                                                                                                                                                                                                                        LPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVD-YGD--TVMYGL 124
                                                                                                                                                                                                                                                                                                                                                                                                                            LPKAFHNGGWGFSALCLLSCALISYGCFVSLITTK-----DKVGVDGYGDMGRILYGP 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTTNNCHNNE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 IIIPF-FVSRAPEHCELVVDL---FVRTVLVCLTCILA-ILIPRLDLVISLVGSVSSSAL 411
                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                              NEDYHDYSSTDVSPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGNIGTGLLG
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                                                                                                                                                                                                                                   Length 692;
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                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                 Query Match 15.7%; Score 388.5; DB 2; Best Local Similarity 28.9%; Pred. No. 1.9e-23; Matches 131; Conservative 76; Mismatches 193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        643 IYIYPPLLHYKASILSGTSRARLLLDLIVIVFG 675
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97; Conserv
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Best Local S
Matches 97
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145 FFLIVT----QLGFCCVYFVFLADNFKQVIEAANGTTNNCHNNETVILTPTMDSRLYMLS 200

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Pypothetical protein T7H20.230 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004 (Speciession: T48239 (Species) (Spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 IQGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIII----PFFVSRAPEHCELV 373
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                                                                                                                                                                                                                                            109 -LFFILLTNMFTEMRIVSFFALVSSVFFVIGAAVIMQYTVQQPNQWDKLPAATNFTGTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 IEAANGTINNCHNNETVILTPIMDSRLYMLSFLPFLVLLVFIRNLRALSIFS---LLANI
                                                                                                                                                                         201 FLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIVQRIPDPSHLPLVAPWKTYPL
                                                                                                                                                                                                                                                                                                                                                                                         261 FFGTAIFSFEGIGMVLPLENKMKDPRKF--PL-ILYLGMVIVTILYISLGCLGYLQFGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 VDLFVRTVLVCLTCILAILIPRLDLVISLVGSVSSSALALIIPPLLEVTTFYSEGMSPLT
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A;Introns: 74/2; 168/1; 234/1; 242/1; 302/1; 375/2; 420/3; 476/1; 490/3;
A;Note: T7H20.230
C;Superfamily: Arabidopsis amino acid transport protein I
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60 YFVNVTILFYQLGMCSVAILFISDNLVNLVGDHLGGT----RHQQMILMATVS-
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A;Rossidues: 1-543 <BEV>
A;Cross-references: UNIPROT:Q9LZL4; UNIPARC:UPI00000A3EF5; 1
A;Experimental source: cultivar Columbia; BAC clone T7H20
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 YRQRMTKIFINLVVWAIGVFAIIAGVYTNIHAIIQSFSQP 387
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E.; Kotani, H.; Tabata, S.; Mew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 HFCRRLNKSFVDYGDTVMYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 LLANITMLVSLV----MIYQFIVQRIPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLP 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LENKMKDPRKFPLILYLGMVIVTILYISLGCLGYLQFGANIQGSITLNLPNCWLYQSVK 336
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           C;Species: Arabidopsis thaliana (mouse-car cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51506
R;Sato, S: Nakamura, Y:; Kaneko, T:; Kato, T:; Asamizu, E:; Kotani, H.; Tak
submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25394
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-426 <SAT>
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                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9LFB3; UNIPARC:UPI00000A18B2; EMBL:AL391147 A;Experimental source: cultivar Columbia; BAC clone F5E19 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 5
A;Introns: 48/1; 247/3
A;Note: F5E19 @
C;Superfamily: Arabidopsis amino acid transport protein I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.1%; Score 274.5; DB 2; 25.9%; Pred. No. 1.7e-14; ive 80; Mismatches 182;
hypothetical protein F5E19_80 - Arabidopsis thaliana
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Best Local Similarity 25.9%
Matches 112; Conservative
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Lybothetical protein T7H20.220 - Arabidopsis thaliana
Cyspeches: Arabidopsis thaliana (mouse-ear cress)
Cyspecies Arabidopsis thaliana
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  341 IGIFFT-YAL---QFYVPAEIIIPFFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRL 396
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                                   SWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTTNNCHNNETVILT
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                                                                                                         DLVISLVGSVSSSALALIIPPLLEVTTF---YSEGMSPLTIFKDALISILGFVGFVVGTY
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Gaps

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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model protein August 24, 2006, 01:16:39; Search time 303 Seconds (without alignments) 1453.160 Million cell updates/sec Run on:

US-10-679-362-2

2469 1 MSTQRLRNEDYHDYSSTDVS......YELIQPSNAPIFINSTCAFI 476 score: Title: Perfect so Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2849598 Total number of hits satisfying chosen parameters:

2849598 segs, 925015592 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

1: uniprot\_sprot:\* 2: uniprot\_trembl:\* UniProt 7.2:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STEMMENTES

|           | ripti | Q7z2h8 homo sapien | Q4r7m7 macaca fasc | Q2vps4 oryctolagus | Q924a5 rattus norv | Q8k4d3 mus musculu | Q5f227 mus musculu | homo         | homo         | homo         | Q8bhk3 m adult mal | Q8jzp1 mus musculu | Q6nra6 xenopus lae | Q8k415 rattus norv | homo         | homo         | homo         | homo         | rattn      | Q495n3 homo sapien | ա ցրա ն      | Q8ch37 mus musculu | Q4s4a7 tetraodon n | Q6zmu7 homo sapien | Q8c077 mus musculu | Q8ch36 mus musculu | Q6ybv0 homo sapien | xenor        | 1 xenor | homo   | 4 homo | Q5r828 pongo pygma |
|-----------|-------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------|--------------|--------------|--------------------|--------------------|--------------------|--------------------|--------------|--------------|--------------|--------------|------------|--------------------|--------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------|---------|--------|--------|--------------------|
| SUMMARIES |       | S36A1 HUMAN        | Q4R7M7 MACFA       | Q2VPS4 RABIT       | S36A1 RAT          | S36A1 MOUSE        | QSF227 MOUSE       | Q495M3_HUMAN | Q6ZWK5 HUMAN | Q7Z6B5_HUMAN | Q8BHK3 MOUSE       | Q8JZP1 MOUSE       | Q6NRA6 XENLA       | Q8K415_RAT         | Q86YK4 HUMAN | Q7Z6B4_HUMAN | Q6ZRU4_HUMAN | Q495N2 HUMAN | Q4V8B1 RAT | Q495N3_HUMAN       | Q811P0 MOUSE |                    |                    | Q6ZMU7 HUMAN       | Q8C077 MOUSE       | Q8CH36_MOUSE       |                    | Q6DDP2_XENLA |         |        |        | Q5R828_PONPY       |
|           | DB    | -                  |                    | 7                  | 7                  | -                  | ~                  | 7            | N            | 7            | 7                  | 7                  | 7                  | 7                  | 7            | 7            | 7            | 7            | 7          | 7                  | 7            | 7                  | ~                  | •                  | •                  | •                  |                    |              | -       | 7      |        | 7                  |
|           | пg    | 476                | 476                | 475                | 475                | 475                | 475                | 483          | 483          | 483          | 478                | 478                | 479                | 481                | 313          | 470          | 470          | 470          | 477        | 511                | 477          | 477                | 490                | 455                | 200                | 200                | 504                | 510          | 522     | 504    | 285    | 301                |
| de        | uery  | 100.0              | 98.8               | 93.9               | 86.9               | 86.7               | 86.7               | 69.8         | 69.4         | 69.3         | 68.8               | 68.7               | 68.4               | 67.9               | 64.5         | 59.8         | 59.8         | 59.6         | 58.7       | 58.6               | 57.4         | 57.3               | 54.7               | 52.7               | 51.7               | 51.3               | 50.9               | ö            | 50.7    | ö      | 43.7   | 43.0               |
|           | Scor  | 2469               | 2439               | 2317.5             | 2146.5             | 2141.5             | 2141.5             |              | 1713.5       | 1711.5       | 1699.5             | 1696.5             | 1689.5             | 1677.5             | 1592         | 1476.5       | 1476.5       | 1472.5       | 1450.5     | 1447               | 1416.5       | 1415.5             | 1351               | 1301               | 1275.5             | 56                 | 1255.5             | 1253         | 1253    | 1244.5 | 1080   | 1060.5             |
|           | 3 Z   |                    | 7                  | m                  | 4                  | 5                  | 9                  | 7            | 80           | 6            | 10                 | 11                 | 12                 | 13                 | 14           | 15           | 16           | 17           | 18         | 19                 | 20           | 21                 | 22                 | 23                 | 24                 | 25                 | 26                 | 27           |         | 29     | 30     | 31                 |

| QBnBs6 homo sapien<br>QBbub0 mus musculu<br>QBmsr2 drosophila<br>Q9vlm3 drosophila<br>Q7ktil drosophila<br>Q744m8 anopheles g<br>Q5f228 mus musculu<br>Q7qf95 anopheles g<br>Q7pm43 anopheles g<br>Q7pm43 anopheles g<br>Q79m43 anopheles g<br>Q79m44 arosophila   |
|--|
| QBNBS6 HUMAN<br>QBBUBO_MOUSE<br>QBWSR2 DROME<br>QYULM3_DROME<br>QYULM4_DROME<br>QYQ4M8_ANOGA<br>QYQ4M8_ANOGA<br>QYQFG5_ANOGA<br>QYPM43_ANOGA<br>QYPM43_ANOGA<br>QYPM43_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA<br>QYOFM45_ANOGA |
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#### ALIGNMENTS

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Ota T., Suzuki Y., Mishikawa T., Otsuki T., Sugiyama T., Irie R.,
Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
B. Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
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M. Yamunco J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
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Abe K., Kamihara K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
Abe K., Kamihara K., Yaku Y., Kodaira H., Murakawa M., Yamazaki M.,
An Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
An Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
A Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
Musashino K., Yuuki H., Oshima A., Saaski N., Aoteuka S.,
A Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
                 O722TB; O727CO; O94M14;

16-AUG-2004, integrated into UniProtKB/Swiss-Prot.

11-AUG-2003, sequence version 1.

01-ACR-2006, entry version 20.

Proton-coupled amino acid transporter 1 (Proton/amino acid transporter 1) (Solute carrier family 36 member 1).
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Intestine;
MEDINE=22564810; PubMed=12809675; DOI=10.1016/S0888-7543(03)00099-5;
BOJI M., Foltz M., Rubio-Aliaga I., Daniel H.;
"A cluster of proton/amino acid transporter genes in the human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen Z., Fei Y.-J., Huang W., Anderson C.M.H., Wake K.A.,
Thwaites D.T., Ganapathy V.;
"Structure and function of a proton-coupled amino acid transporter
(hPAT1) cloned from the human intestinal cell line Caco2.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Endometrial tumor;
The German cDNA consortium;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND FUNCTION
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    476 AA.
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NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1)
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    PRT;
                                                                                                                                                                                                                                                                                       Name=SLC36A1; Synonyms=PAT1;
Homo sapiens (Human).
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse genomes.";
Genomics 82:47-56(2003).
[3]
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S36A1 HUMAN
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Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kunngai A., Takemoto M., Kawakami B., Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fuji Y., Ozaki K., Hirao M., Ohmori Y., Akawakami T., Nogatake N., Inagami A., Ohmori Y., Okitani R., Kawakami T., Nogatake N., Inch T., Shigeta K., Senba T., A Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Tagashi T., Oyama M., Hara H., Watanabe M., Komatsu T., Okumura M., Hara H., Watanabe M., Kamatsu T., Okumura K., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Complete sequencing and characterization of 21,243 full-length human CDNAS.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                           FUNCTION: Neutral amino acid/proton symporter. Has a pH-dependent electrogenic transport activity for small amino acids such as glycine, alanine and proline. Besides small amino acids, it also recognize their D-enantiomers and selected amino acid derivatives such as gamma-aminobutyric acid (By similarity). SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal and plasma membrane (By similarity).

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid transporter 1.
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HGNC; HGNC:18761; SLC36A1.

MIN; 606661; gene.

InterPro; IPR003422; AA/rel permease2.

InterPro; IPR013057; AA_transpt_TM.

Pfam; PF01490; Aa_transpt_TM.

AAlternative splicing; Anino-acid transport; Glycoprotein; Membrane; Symport; Transmembrane; Transport
                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=0722H8-2; Sequence=VSP 011314;
Note=No experimental confirmation available;
SIMILARITY: Belongs to the amino acid/polyamine transporter 2
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V -> A (in Ref. 4).
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-> L (in Ref. 1).
-> G (in Ref. 1).
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EMBL; AX162213; AA011197.1; -; mRNA.
EMBL; BX537963; CAD97927.1; -; mRNA.
EMBL; AK057340; BAB71435.1; -; mRNA.
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Distributed under the Creative Commons Attribution-NoDerivs License
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19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 5.
Testis cDNA, clone: QtsA-14/98, similar to human solute carrier family 36 (proton/amino acid symporter), member 1 (SLC36Al),.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
Pubmed=1594441; DOI=10.1093/molbev/msi187;
Pubmed=1594441; DOI=10.1093/molbev/msi187;
Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.;
Substitution Rate and Structural Divergence of 5'UTR Evolution:
"Substitution Rate and Structural Divergence of 5'UTR Evolution:
Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.";
Mol. Biol. Evol. 22:1976-1982(2005).
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                                               Length 476;
Q -> R (in Ref. 4).
; 628AE7FC7A6559F0 CRC64;
                                             ; Score 2469; DB 1;
; Pred. No. 9.6e-171;
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Q4R7M7;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miyauchi S., Abbot E.L., Zhuang L., Subramanian R.K., Ganapathy V. Thwaites D.T.; "Isolation and function of rabbit PAT1 (slc36al) and coexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTTFYSEGMSPLTIFKDALISILGFVGFVVGTYEALYELIQPSNAPIFINSTCAFI
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
InterPro; IPR002422; AA/rel_permease2.
Pfam; PF01490; Aa_trans; 1.
PRQUENCE 476 AA; 53063 MW; 6485B3BBF84CEEF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the IMINO transporter in renal brush-border membrane vesicles."; Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
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SEOUENCE 475 AA; 52701 MW; A66BB738C7D2B27F CRC64;
                                                                                                              .4e-168;
                                                                                             98.8%; Score 2439; DB 2;
llarity 98.3%; Pred. No. 1.4e-168;
Conservative 5; Mismatches 3:
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07-FEB-2006, entry version 3.
Proton/amino acid transporter 1.
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NCBI_TaxID=9986;
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Q2VPS4;
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DB 2; Length 475;

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Query Match

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Mammalia; Eutheria; Euarchontoglires, Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                 Gaps
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Reimer R.J., Edwards R.H.;
"The H+-coupled electrogenic lysosomal amino acid transporter LYAATI
localizes to the axon and plasma membrane of hippocampal neurons.";
J. Neurosci. 23:1265-1275(2003).
-!- FUNCTION: Neutral amino acid/proton symporter. Probably involved
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MEDLINE=21309917; PubMed=11390972; DOI=10.1073/pnas.121183498;
Sagne C., Agulhon C., Ravassard P., Darmon M., Hamon M.,
El Mestikawy S., Gasnier B., Giros B.;
"Identification and characterization of a lysosomal transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, SUBCELLULAR LOCATION, AND
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                                 Indels
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                9.3e-160;
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                                 Mismatches
                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Slc36a1; Synonyms=Lyaat1, Pat1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence version 1. entry version 23.
92.2%; P1.
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                               439; Conservative
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PubMed=12598615;
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361 FFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLDLVISLVGSVSSSALALIIPPLLE 420
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                             $\overline{8.96A1}$ MOUSE STANDARD; PRT; 475 AA. $\overline{0.84A15}$, Q8A103. $\overline{0.84A15}$, Q8A104. $\overline{0.84A10}$, integrated into UniProtKB/Swiss-Prot. $\overline{0.84A10}$, sequence version 1. $\overline{0.84A10}$, entry version 21. $\overline{0.84A10}$, entry version 21. $\overline{0.84A10}$, Proton-coupled amino acid transporter 1 (Proton/amino acid transporter 1) (Solute carrier family 36 member 1).
                                                                                              300 VLYISLGSLGYLQFGADIKGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVAAEIIIP
                                                                                                                                                                                        360 AIVSRVPERFELVVDLSARTAMVCVTCVLAVLIPRLDLVISLVGSVSSALALIIPPPLLE
                                                                       301 ILYISLGCLGYLQFGANIQGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mamm. Genome 15:114-125(2004).
-!- FUNCTION: Neutral amino acid/proton symporter. Has a pH-dependent
                                                                                                                                                                                                                                                                            420 VTTYYGEGISPLTITKDALISILGFVGFVVGTYESLWELIQPSHSDSSTNSTSAF1 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             electrogenic transport activity for small amino acids such as glycine, alanine and proline. Besides small apolar L-amino acids, it also recognize their D-enantioners and selected amino acid derivatives such as gamma-aminobutyric acid.
SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasma membrane (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJNE-22063354; PubMed=11959859; DOI=10.1074/jbc.M200374200;
Boll M., Foltz M., Rubio-Aliaga I., Kottra G., Daniel H.;
"Functional characterization of two novel mammalian electrogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=15058382; DOI=10.1007/s00335-003-2319-3; Bermingham J.R. Jr., Pennington J.; "Organization and expression of the SLC36 cluster of amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLECTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY
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EMBL; AY211262; AA037090.1; -; mRNA.
EMBL; AX211262; AA037090.1; -; mRNA.
Ensembl; ENSMTGG0000020261; Mus musculus.
MGI; MGI:2445299; SlG3641.
GO; GO:0015187; F:glycine transporter activity; IDA.
GO; GO:0015180; F:L-alanine transporter activity; IDA.
GO; GO:0015180; F:L-proline transporter activity; IDA.
GO; GO:0015808; P:L-proline transport; IDA.
GO; GO:0015808; P:L-proline transport; IDA.
GO; GO:0015824; P:L-proline transport; IDA.
GO; GO:0015924; P:L-proline transport; IDA.
GO; GO:0015924; P:L-proline transport; IDA.
GO; GO:0015924; P:L-proline transport; IDA.
InterPro; IPR002422; AA/rel_permease2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Slc36al; Synonyms=Patl;
Mus musculus (Mouse).
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           in the efflux of lysosomal proteolysis products such as L-proline, Lalanine and glycine from the cell. May play a role in specifying sites for exceytosis in neurons.

SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal and
                                                                                              plasma membrane. In neurons, colocalizes with the exocyst complex in the axonal processes.

TISSUE SPECIFICITY: Widely expressed and predominantly expressed in brain. Within the brain, expression restricted to neurons and not detected in glial cells. Abundant in regions rich in neurons using glutamate and GABA such as Purkinje cells in the cerebellum and pyramidal cells in the hippocampus.

SIMILARITY: Belongs to the amino acid/polyamine transporter 2
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Pfam; PF01490; Aa_trans; 1.
Amino-acid transport; Glycoprotein; Membrane; Symport; Transmembrane;
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-GO; GO:0005764; C:1ysosome; IDA.
-GO; GO:0005868; C:plasma membrane; IDA.
GO; GO:0015078; F:nydrogen ion transporter activity; IDA.
GO; GO:0015175; F:neutral amino acid transporter activity; IDA.
GO; GO:0015904; P:neutral amino acid transport; IDA.
GO; GO:001592; P:proton transport; IDA.
InterPro; IPR002422; AA/rel_permease2.
InterPro; IPR013057; AA transpt TM.
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Ensembl; ENSRNOG00000012356; Rattus norvegicus
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nes 408; Conservative
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Amino-acid transport; Glycoprotein; Membrane; Symport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                    Proton-coupled amino acid transporter /FTId=PRO 000093826.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-2005, integrated into UniProtKB/TrEMBL.
10-MAY-2005, sequence version 1.
07-FBB-2006, entry version 4.
Solute carrier family 36 (Proton\/amino acid symporter), member 1.
Name-Slc36a1; ORFNames=RP24-239D8.3-001;
Mus musculus (Mouse).
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(Potential).
(Potential).
(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                                            86.7%; Score 2141.5; DB 1; Length
85.9%; Pred. No. 5.5e-147;
ive 33; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                    -> S (in Ref. 2).
-> P (in Ref. 2).
113C23309F2B51F1 CRC64;
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InterPro, IPR013057; AA_transpt_TM
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Matches 409; Conservative
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175 AA;
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QSF227;
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                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSTQRLRNEDYHDYSSTDVSPEESPSEGLGSF-SPGSYQRLGENSSMTWFQTLIHLLKGN
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              Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                             EMBL, AL713870; CAIS2048.1; -; Genomic DNA.
Ensembl; ENSMUSGO000020261; Mus musculus.
GO; GO:0016020; C:membrane; IBA.
GO; GO:0005279; F:amino acid-polyamine transporter activity; J
GO; GO:0006865; P:amino acid transport; IEA.
InterPro; IPR002422; AA/rel_permease2.
InterPro; IPR013057; AA_transpt_TM.
Pfam; PR01490; AA transpt_TM.
ERQUENCE 475 AA, 52466 MW; 113C233309F2B5IF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length
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                                                                                                                                                     Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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es 33;
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Pred. No. 5.56
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                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                     NCBI_TaxID=10090;
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            TUSUEEPCR rescued clones;

TISSUE=PCR rescued clones;

RA TISSUE=PCR rescued clones;

RA MILE 22388257; PubMed=12477912; DOI=10.1073/pnas.242603899;

RA STRAUSPER R.L., Feligold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhar N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhar N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M.J., Dardan H., Bonaldo M.F., Gasvant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Maket J.A., Gunzardre P.H.,

RA Rochards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAKKLENKD----STFL--DESPSESAGLK------KTKGITVFQALIHLVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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EMBL; BC101101; AA101102.1; -; mRNA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:00058279; F:amino acid-polyamine transporter activity; IEA.

GO; GO:0006865; P:amino acid transport; IEA.

InterPro; IPRO02422; AA/rel_permease2.

Pfam; PF01490; Aa_trans; 1.

PEQUENCE 483 AA, 53216 MW; E283B8GGF0C63666 CRC64;
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Pred. No. 1.4e-116;
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71.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 VQRIPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIV 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 SAKKLENKD-----STFL--DESPSESAGLK-------KTKGITVFQALIHLVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F. Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Ishii S., Yamamoto J., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kimura H., Kanda K. Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A. Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Sugano S., Nagahari K., Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
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Ensembl, ENSG00000186335; Homo sapiens.
HGNC; HGNC:1.8762; SLC36A2.
GO; GO:0016202; C:membrane; IEA.
GO; GO:0016202; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
InterPro; IPR003422; AA/rel_permease2.
InterPro; IPR01357; AA_rel_permease2.
                              427 EVTTFYSEGMSPLTIFKDALISILGFVGFVVGTYQALDELLKSEDSHPFSNST
EVITFYSEGMSPLTIFKDALISILGFVGFVVGTYEALYELIQPSNAPIFINST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Mismatches
                                                                                                                                                                                                           483
                                                                                                                                                                                                                                                                                                 05-JUL-2004, sequence version 1.
21-FEB-2006, entry version 13.
CDNA FLJ16051 fis, clone KIDNE2000832.
                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 71.5
Matches 338; Conservative
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                                                                                                                                                                                                                                                                                                                                                CDNA FLJ16051 fis, clo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TaxID=9606;
                                                                                                                                                                                                           QEZWKS HUMAN
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PRT;
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07-FEB-2006, entry version 24.
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                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                   307
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QBHK3 MUUSE
QBHK3 MUUSE
DC QBHK3 MUUSE
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DE Clone:93:00
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807 TSLYIGMAALGYLRFGDDIKASISLNLPNCWLYQSVKLLYIAGILCTYALQFYVPAEIII 366
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                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22694810; PubMed=12809675; DOI=10.1016/S0888-7543(03)00099-5;
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                                                                                                                                          Boll M., Foltz M., Rubio-Aliaga I., Daniel H.; A cluster of proton/amino acid transporter genes in the human and
                                                                                                                     EVITTYSEGMSPLTIFKDALISILGFVGFVVGTYEALYELIQPSNAPIFINST 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016020; C:membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006859; P:amino acid-polyamine transport:
InterPro; IPR002422; AA/rel_permease2.
InterPro; IPR013057; AA_rranspt_TM.
Pfam; PF01490; Aa_transpt_TM, 92E8CEGC38F56673 CRC64;
SEQUENCE 483 AA, 53227 WW; 92E8CEGC38F56673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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                                                                                                                                                                                                                                                                                                         integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                    483 AA
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Ensembl; ENSG0000186335; Homo sapiens.
LinkHub; Q7Z6B5; -.
                                                                                                                                                                                                                                                                                                                          01-OCT-2003, sequence version 1.
07-FEB-2006, entry version 14.
Proton/amino acid transporter 2.
                                                                                                                                                                                                                                                                                                                                                                                        Name=SLC36A2; Synonyms=PAT2;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                  PRELIMINARY;
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Matches 339; Conservative
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Q726B5;
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RC STRAIN-C57BL/63, and NOD; TISSUE-Activated spleen, Aorta and vein, RC Diencephalon, and Whole body;
RX PubMed-E1611186/science.1112014;
Ry PubMed-E16141072; DOI=10.1186/science.1112014;
Ry PubMed-E16141072; DOI=10.1186/science.1112014;
RA Salic V.B. B. Brenner S.B.; Batalov S., Fortest A.R., Zavolan M., Balic V.B., Brenner S.B.; Batalov S., Fortest A.R., Zavolan M., Bayis M.J., Wilming L.G., Aidnins V., Allen J.E.,
Ry Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., RA Bansal M., Barter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., RA Bansal M., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., RA Tetcher C.F., Fukushima T., Frunno M., Futaki S., Raziboli M., RA Tetcher C.F., Fukushima T., Frunno M., Futaki S., Hishkawa T., Ratano H., Kalon B., Lancon M., Ikeo K., Iwama A., Ishkawa T., Ratano H., Kalon B., Mayashi Y., Henson T.R., Hishkawa T., Ratano H., Kalon B., Razaerevic D., Lipovich L., Liu J., Liu J., Liu S., Mulliam S., Madan Babu M., Madera M., Marchinn S., Muller N., Makano M., Nakauchi H., Na P., Nataki S., Nalider N., Nakauchi H., Na P., Nataki M., Ravaski S., Noris S., Radalin A., Schneider C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Radonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
                                              366
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|| :|| PPAISRVSTRWALPLDLSIRLVWVCLTCLLAILIPRLDLVIPLVGSVSGTALALIIPPLL
                                                                                                                            PFFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLDLVISLVGSVSSSALALIIPPLL
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Aorta and vein,
Diencephalon, and Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                       420 EVITFYSEGMSPLTIFKDALISILGFVGFVVGTYEALYBLIQPSNAPIFINST 472
                                                                                                                                                                                                                                                                                                                                           Name=Slc36a2, Synonyme=Tramd1, ORFNames=RP24-239D8.1-001, Mus musculus (Mouse).
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"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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NUCLECTIVE SEQUENCE:

C STRAIN-C57BL/6J, and NOD; TISSUE-Activated spleen, Aorta and vein, C Diencephalon, and NOD; TISSUE-Activated spleen, Aorta and vein, C Diencephalon, and NOD; TISSUE-Activated spleen, Aorta and vein, C Diencephalon, and Whole body;

RX MISAIGO I., Osato N., Saito R., Suzuki H., Yamanaka I., Kayosawa H., RA Okazaki Y., Fararu M., Bato R., Suzuki H., Yamanaka I., Kiyosawa H., RA Baidarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Baidarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Baidarelli R., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Blake J.A., Rawaji H., Kawasawa Y., Kedzierski R.M., Frazer K.S., RA Garsterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Ramai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Arnai A., Kawaji H., Kawasawa Y., Kedzierski R.M., Kang B.L., Andajott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., RA Nagashima T., Numata K., Okido T., Pavan W.J., Pamandaran S., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandan S., Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K., Mang Y., Watanabe Y., Wall R., Wall M., Taylor M.S., Teasdale R.D., Tomita M., Taylor M., Xang L., Harbizume W., Imbata K., Takhani Y., Itoh M., Kagawa I., R., Hara A., Hashizume W., Imbata K., Ishing W., Anakawa T., Fukuda S., Haraki T., Waki K., Sasaki D., Shibata K., Shinagawa A., Rahara A., Hashizume W., Imbata K., Ishing K., Shinagawa A., Malaneshi A., Soshino M., Waterston R., Ender S., Rogers J., R., Barney B. Hayashizaki X., Shinagawa A., Malanishi A., Soshino M., Waterston R., Lander E.S., Rogers J., R., Barney B., Hayashizaki Y., Shinagawa A., Harana A., Har
Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K., Tamg S., Taylor M.S., Tagner J., Teichmann S.A., Ubeda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Grimmond S.M., Teasdale R.D., Liu E.T., Rarisic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Eukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki B., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
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"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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STRAIN—CSTBL/64, and NoD; TISSUE=Activated spleen, Aorta and vein, Diencephalon, and Whole body;

MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLECTIDE SEQUENCE. STRAIN-CSTBL/6J, and NOD; TISSUE-Activated spleen, Aorta and vein, Diencephalon, and Whole body;
Diencephalon, and Whole body;
Pubmeda-16141073; DOI-10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
                                                                                                                                                                                                                                                                                                                                                                                                           "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563 (2005).
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NUCLECTIDE SEQUENCE.

STRAIN=FVBN/K; ISSUE=Salivary gland;
STRAIN=FVBN/K; TISSUE=Salivary gland;
STRAIN=FVBN/K; TISSUE=Salivary gland;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., STRANN=CSTBL/66; TISSUE-Aorta and vein;
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
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Hayashida K., Hayatsu W., Hiramoto K., Hiraoka T.,
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Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. STRAIN=CSTBL/6J, and Whole body; DissuB=Activated spleen, Aorta and vein, Diencephalon, and Whole body; MEDLIRE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Shibata K., Itoh M., Forno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Shibata K., Itoh M., prepare full-length cDNA ibraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000). Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Tagami M. Shibate K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sunin N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ozawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000). STRAIN=CS7BL/6J, and NOD; TISSUE=Activated spleen, Aorta and vein, Diencephalon, and Whole body; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. 

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Gaps

7;

68.8%; Score 1699.5; DB 2; Length 478; llarity 72.6%; Pred. No. 6.4e-115; Conservative 50; Mismatches 67; Indels 7;

Best Local Similarity Matches 329; Conserv

Query Match

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NCBI_TaxID=8355
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                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6; TISSUE=Pou3f1 mutant sciatic nerves; MEDLINE=22338849; PubMed=12451123; Bermingham J.R. Jr., Shumas S., Whisenhunt T., Sirkowski E.E., O'Connell S., Scherer S.S., Roaneld M.G.; Scherer S.S., Roanes that are downregulated in the absence of the POU domain transcription factor pou3f1 (Oct-6, Tst-1, SCIP) in sciatic
                    | : ||: ||: || || |||||||||| sQDPSPANGSSSESSK-----KTKGITGFQTLVHLVKGNMGTGILGLPLAVKNAGILM
                                                                                                            SPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGNIGTGLLGLPLAVKNAGIVM
                                                                                       GPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTVMYGLESSPCSWLRNHAHWG
                                                                                                                                                                                                                                                                SFLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIVQRIPDPSHLPLVAPWKTYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=SIC36a2; Synonyms=PAT2, Tramd1;
*Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
*Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognath1;
*Muroidea; Muridae; Murinae; Mus.
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MEDLINE-22063154; PubMed=11959859; DOI=10.1074/jbc.M200374200;
MEDLINE-22063154; PubMed=11959859; DOI=10.1074/jbc.M200374200;
Boll M., Foltz M., Rubio-Aliaga I., Kottra G., Daniel H.;
Functional characterization of two novel mammalian electrogenic Proton-dependent amino acid cotransporters.";
J. Biol. Chem. 277:22966-22973(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 ISILGFVGFVVGTYEALYELIQPSNAPIFINST 472
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07-FEB-2006, entry version 16.
Tramdorin 1 (Proton/amino acid transporter 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002, integrated into UniProtKB/TrEMBL
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Ensembl; ENSMUSG0000020264; Mus musculus.
MGI; MGI:1891430; Slc36a2.
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R GO; GO:0016021; C:integral to membrane; RCA.
R GO; GO:0005886; C:plasma membrane; IDA.
R GO; GO:0005886; C:plasma membrane; IDA.
R GO; GO:0005187; F:glycine transporter activity; IDA.
GO; GO:0015187; F:glycine transporter activity; IDA.
GO; GO:0015180; F:hydrogen:amino acid symporter activity; IDA.
R GO; GO:0015193; F:L-alanine transporter activity; IDA.
R GO; GO:0015193; F:L-proline transporter activity; IDA.
R GO; GO:0015886; P:L-proline transport; RCA.
R GO; GO:0015886; P:L-proline transport; IDA.
R GO; GO:0015824; P:L-alanine transport; IDA.
R GO; GO:0015824; P:L-proline transport; IDA.
R HICEPPRO; IPR013057; AA_transport
R InterPro; IPR013057; AA_transpt_TM.
R Ffam; PF01490; Aa_transpt_TM.
R Ffam; PF01490; Aa_transpt_TM.
R Ffam; PF01490; Aa_transpt_TM.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.7%; Score 1696.5; DB 2, 72.6%; Pred. No. 1.1e-114; ive 49; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 ISILGFVGFVVGTYEALYELIQPSNAPIFINST 472
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|SILGFMGFVVGTYQALDELIKSGNSPALSNST 474
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QGNRAG;
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J., Abrakson R.D., Mullahy S.J., Abrakson R.D., Mullahy S.J., Abrakson R.D., Mullahy S.J., Abraholo D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Avillaton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Abraholo D.K., Muzny D.M., Garcia A.M., Gay L.J., Hulyk S.W., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Abraholo D. Dickson M.C., Rodriguez S., Sanchez A., Miting M., Andan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A.; Schein J.E., Jones S.J.M., Marra M.A.; and mouse DNA schemators H. Schein J.E., Jones S.J.M., Marra M.A.; and mouse DNA schemators H. Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC070857; AAH70857.1; -; mRNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
InterPro; IPR002422; AA/rel_permease2.
InterPro; IPR002422; AA/rel_permease2.
PEm; PF01490; Aa_transpt_TM.
PEm; PF01490; Aa_transpt_TM.
SEQUENCE 479 AA; S3309 MW; 4AF813EA7766ADE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein S., Strausberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches 320, Conservative
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TISSUE=Oocytes;
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320 GSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIPFFVSRAPEHCELVVDLFVR 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 LFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVTILYISLGCLGYLQFGANIQ 319
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359 IPFFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLDLVISLVGSVSSSALALIIPPL 418
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                                                                                                                                                          421 LEILTYYTEGLSRWVIAKDIFISLVGFLGFVLGTYVALWELIVPEVSPA-LNETALFV 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley;
MEDLINE=22338849; PubMed=12451123;
MEDLINE=22338849; PubMed=12451123;
Bermingham JR. Jr., Shumas S., Whisenhunt T., Sirkowski E.E.,
O'Connell S., Scherer S.S., Rosenfeld M.G.;
"Identification of genes that are downregulated in the absence of the POU domain transcription factor pou3fl (Oct-6, Tst-1, SCIP) in sciatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 SPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGNIGTGLLGLPLAVKNAGIVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rattus norvegicus (kat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                            419 LEVITFYSEGMSPLTIFKDALISILGFVGFVVGTYEALYELIQPSNAPIFINSTCAFI
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SEQUENCE 481 AA; 52278 MW; FBCB4C32BCB0BB12 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ensembl. ENSRNOG0000011892; Rattus norvegicus. RGD; 620492; Slc36a2. GG; GO:0015187; Fglycine transporter activity; InterPro; IPR003422; AA/rel permease2.
                                                                                                                                                                                                                                                                                                                                                              integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                           481 AA
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                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                           sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Slc36a2; Synonyms=Tramd1;
                                                                                                                                                                                                                                                                                                                                  Q8K415;
01-0CT-2002, integrated into U
01-0CT-2002, sequence version
07-FEB-2006, entry version 11.
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Les 325; Conservative
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                                                               ANITMLVSLVMIYQFIVQRIPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPRKFPLILYLGMVIVTILYISLGCLGYLQFGANIQGSITLNLPNCWLYQSVKLLYSIGI 343
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325 ASITLNLPNCWLYQSVKLLYVVGILCTHALQFYVPAEIIIPLAVSQVSKRWALPVDLSIR 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 DNFKQVIEAANGTTNNCHNNETVILIPPMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSVSSSALALIIPPLLEVTTFYSEGMSPLTIFKDALISILGFVGFVVGTYEALYELIQPS
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Ensembl; ENSG00000123643; Homo sapiens.
GO; GO:0016021; .c.integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:001620; C:membrane; IEA.
GO; GO:00065279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
InterPro; IPR002422; AA/rel_permease2.
InterPro; IPR013057; AA/rel_permease2.
Pfam; PF01490; Aa_transpt_TW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15058382; DOI=10.1007/s00335-003-2319-3; Bermingham J.R. Jr., Pennington J.; "Organization and expression of the SLC36 cluster of amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .64.5%; Score 1592; DB 2; Length 313; 100.0%; Pred. No. 2.6e-107; ative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                    440 ISILGFVGFVVGTYEALYELIQPSNAPIFINST 472
                                                                                                                                                                                                                                    01-JUN-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                            313 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane transport protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mamm. Genome 15:114-125(2004).
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Best Local Similarity 100.
Matches 313; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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Q86YK4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=SLC36A1;
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10 086YK HUM
10 086YK
AC 086YK
AC 086YK
AC 086YK
AC 086YK
AC 01-JT
DT 01
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TISSUE=PCR rescued clones;

NUCLECATIDE SEQUENCE.

TISSUE=PCR rescued clones;

MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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Alsenis S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Robkins R.F., Jordan H., Moore T.B., Tonylynki S., Carninci P., Prange C.,

Reha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robkins S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rochards A., Young A. C., Garcia A.M., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A. C., Shevchenko Y., Boutfard G.G.,

Rochiquez A.C., Grimwood J.W., Schmutz J., Myers R.M.,

Rochiquez A.C., Grimwood J.W., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Rochicutticial A., Schein J.E., Jones S.J.M., Marra M.A.;

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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Rochicutticial A., Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-22694010; PubMed=12809675; DOI=10.1016/S0888-7543(03)00099-5; Boll M., Foltz M., Rubio-Aliaga I., Daniel H.; "A cluster of proton/amino acid transporter genes in the human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016020; C:membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
InterPro; IPR003422; AA/rel_permease2.
InterPro; IPR013057; AA_transpt_TM.
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SEQUENCE 470 AA; 51735 MW; AA192584E6BFE848 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carrier
                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003, integrated into UniProtKB/TrEMBL 01-OCT-2003, sequence version 1. 07-EB-2006, entry version 17. Proton/amino acid transporter 3 (Solute carriv
                                                                                                                                                                                                                                                                                         470 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Proton/amino acid symporter), member 3)
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EMBL; BC101095; AAI01096.1; -; mRNA.
Ensembl; ENSG00000186334; Homo sapiens.
                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                         PRELIMINARY;
464 NAPIFINSTCAFI 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse genomes.";
Genomics 82:47-56(2003).
                                           301 NAPIFINSTCAFI
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                                                                                                                                                                                                                                                                                         Q7Z6B4_HUMAN
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59.8%; Score 1476.5; DB 2; Length 470;

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LLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTVMYGL 124
                                                                                              TVILTPTMDSRLYMLSFLPPLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIVQRIP 244
                                                                                                                                            240 YPSNLPLANANWKTFLLFFGTAIFTFEGVGMVLPLKNQMKHPQQFSFVLYLGMSIVIILYI 299
                                                                                                                                                                                                                   245 DPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVTILYI 304
                                                                                                                                                                                                        305 SLGCLGYLQFGANIQGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIPFFVS 364
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                                         59
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Matches 291; Conservative 77; Mismatches 95; Indels
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Scoring table:

Searched:

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Perfect score:

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Sequence 31761, A Sequence 46978, A Sequence 27, Appl Sequence 27, Appl Sequence 11556, A Sequence 1287, Appl Sequence 37, Appl Sequence 37, Appl Sequence 43616, A Sequence 40, Appl Sequence 530, Appl Sequence 531, Appl Sequence 47931, A Sequence 530, Appl Sequence 47931, Appl Sequence 523, Appl Sequence 530, Appl Sequence 530, Appl Sequence 54, Appli Sequence 523, Appli Sequence 523, Appli
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                                         US-09-370-253-2

US-09-640-419C-27

US-09-919-407-11556

US-09-919-016-11556

US-09-178-093B-28

US-09-270-767-42974

US-09-270-767-42974

US-09-270-767-43616

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US-09-583-110-5223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3076, Application US/10094749
Patent No.-6979557
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
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Best Local Similarity 90.8'
Matches 432; Conservative
       TYPE: PRT
CORGANISM: Homo sapiens
US-10-094-749-3076
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Sequence 20813, A
Sequence 20813, A
Sequence 10, Appl
Sequence 6, Appli
Sequence 32811, A
Sequence 32811, A
Sequence 25, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence 92, Appl
Sequence 1, Appli
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                                                                                                                                                                 August 24, 2006, 01:25:09; Search time 50 Seconds (without alignments) 833.292 Million cell updates/sec
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1 MSTQRLRNEDYHDYSSTDVS......YELIQPSNAPIFINSTCAFI 476
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/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
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/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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                               GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-09-178-03B-1
US-09-178-03B-2
US-08-362-512A-2
US-08-964-939-2
US-09-854-799-2
US-09-854-796A-20815
US-09-248-796A-20815
US-09-248-796A-20815
US-09-248-796A-20815
US-09-248-796A-20815
US-09-270-767-4308
US-09-270-767-48028
US-09-270-767-48028
US-09-270-767-48028
US-09-864-739-4
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US-09-864-739-4
US-09-976-594-584
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US-09-640-419C-26
US-09-248-796A-20822
US-09-640-419C-5
US-09-311-021-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                            650591 seqs, 87530628 residues
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                                                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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APPLICANT: Curtis, Rory A.J.
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Meyers, Rachal E.
TILLE OF INVENTION: NOVEL 38594, 57312, 53659, 67250, 63760, 49938, 32146,
TITLE OF INVENTION: 57259, 67118, 67067, 62092, 8099, 46455, 54414, 53763,
TITLE OF INVENTION: 67076, 67102, 44181, 67084FL, 67084ALT, FBH58295FL, 57255,
TITLE OF INVENTION: AND 572531t MOLECULES AND USES THEREFOR
FILE REFERENCE: MAI-249
CURRENT APPLICATION NUMBER: US/10/154,419
CURRENT FILING DATE: 2002-05-22
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FRASESQ Version 4.0
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                                                                                                                                       315 YISLATLGYMCFRDBIKGSITLNLPQDWMLYQSVKILYSFGIFVTYSIQPYVPAEIIIPA 374
                                                                                                                                                                                                             362 FVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLDLVISLVGSVSSSALALIIPPLLEV 421
                                                                                                                                                                                                                                     422 TTFYSEGMSPLTIFKDALISILGFVGFVVGTYEALYELIQPSNA------PIFINST 472
                                                                                                                                                                                                                                                                                                                              | : : : |: |: || || || : : || || || 435 LIFSKDHYNV#WYLKNISIAFTGFVGFLLGTYVTVEEIIYPTTAVADGASQSLSLANVNST 494
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                        IPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVTIL 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 MGIVTTLYVTLATLGYMCFHDEIKGSITLNLPQDVWLYQSVKILYSFGIFVTYSIQFYVP 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WVIVTILYISLGCLGYLQFGANIQGSITLNLP-NCWLYQSVKLLYSIGIFFTYALQFYVP 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.9%; Score 1255.5; DB 2; Length 485; 52.0%; Pred. No. 1.8e-121;
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; Sequence 92, Application US/10154419
; Patent No. 6972187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52.0%
Matches 254; Conservative
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LENGTH: 485
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                                                                                                                                                                 HNNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIV 240
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                                                                      361 FFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLDLVISLVGSVSSSALALIIPPLLE 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTT---NNCHN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSQVCERRSVDLRVYMLCFLPLLILLVFIRELKSLFVLSFLANISMAASLVIIYQYVVRS 254
                                                                                                                                       HNNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIV
                                                                                                                                                                                                                                                                                                                            ILYISLGCLGYLQFGANIQGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 LINEQNFDGSS-----DEEQEQTL--LPMQKHYQLDGQ-HGISFVQTLMHLLKGNIGTGL
IGTGLLGLPLAAKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTV
                                                                                                                                                                                                                                  QRIPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VITFYSEGMSPLTIFKDALISILGFVGFVVGTYEALYELIQPSNAPIFINSTCAFI 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VITFYSEGMSPLIIFKDALISILGFVGFVVGTYEALYELIRPSNAPIFINSTCAF1 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: synthetic peptide (RVT2 polypeptide sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80; Mismatches 117; Indels
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APPLICANT: Richard J. Reimer
APPLICANT: Stevet L. McIntire
APPLICANT: Steve L. McIntire
APPLICANT: Steve L. McIntire
APPLICANT: Steve L. McIntire
APPLICANT: Kim Schuske
ITILE OF INVENTION: Vesicular Amino Acid Transported
ITILE OF INVENTION: Composition and Method
FILE REFERENCE: 2002-0005.30
CURRENT APPLICATION NUMBER: US/09/178,093B
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 00/063,012
PRIOR FILING DATE: 1997-110-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.4%; Score 1293.5; DB 2; 54.7%; Pred. No. 2.2e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/09178093B Patent No. 6660846
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 54.78
Matches 263; Conservative
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US-09-178-093B-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 ---MYNS-----FPGLPVSQKSWSIIATAVLLPCAFLKNLKAVSKFSLLCTLAHFVINIL 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387 VAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPACYGGDGRLKSWGLTLRCALVVFTLLM
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                                             397 DLVISLVGSVSSSALALIIPPLLEVTTFYSEGMSPLTIFK---DALISILGFVGFVVGTY
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                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Robert H. Edwards
APPLICANT: Robert H. Edwards
APPLICANT: Richard J. Reimer
APPLICANT: Richard J. McIntire
APPLICANT: Erik M. Jorgenson
APPLICANT: Kim Schuske
TITLE OF INVENTION: Vesicular Amino Acid Transported
TITLE OF INVENTION: Composition and Method
FILE REFERENCE: 2002-0005.30
CURRENT PAPLICATION NUMBER: US/09/178,093B
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/063,012
PRIOR APPLICATION NUMBER: 60/063,012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.3%; Score 229.5; DB 2; Best Local Similarity 22.0%; Pred. No. 6.6e-15; Matches 95; Conservative 82; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , LOCATION: (1)...(525)
, OTHER INFORMATION: RUNC-47 polypeptide sequence US-09-178-093B-2
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 525
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; Patent No. 6660846
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                                                                                                                                  454 EALYELIQPSNA 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LSFVSQWSFSTITFSLNINTLPTIVGMVVFGYTSHIFLPNLEGNMKNPAQFNV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 ILYLGMVIVTILYISLGCLGYLQFGANIQGSITLNLPNCWLYQSVKLLYS----IGIFFT 346
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                            414
                                                    115 IPPLLEVTTFYSEGMSPLTIFKDALISILGFVGFVVGTYEALYELIQPS-----NAP 466
                                                                                                                                         77 IVMGPISLLIIGIVAVHCMG---ILVKCAHHFCRRLNKSFVDYGDTVMYGLESSPCSWLR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 NHAHWGRRVVDFF-----LIVTQ----LGFCCVYFVFLADNFKQVIEAANGTTNNCHN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 -----REIADFYKPGFGKWVLAAQLTELLSTCIIYLVLAAD------LLQSCF- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 NETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANIT-MLVSLVMIYQFIVQ 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Robert H. Edwards
APPLICANT: Richard J. Reimer
APPLICANT: Steve L. McIntaire
APPLICANT: Steve L. McIntaire
APPLICANT: Kim Schuske
TITLE OF INVENTION: Vestcular Amino Acid Transported
TITLE OF INVENTION: Composition and Method
TITLE OF INVENTION: Composition and Method
FILE REFERENCE: 2002-0005.30
CURRENT APPLICATION NUMBER: US/09/178,093B
CURRENT FILING DATE: 1997-10-23
PRIOR FILING DATE: 1997-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CHAIN
LOCATION: (1)...(486)
OTHER INFORMATION: UNC-47 polypeptide sequence
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09178093B
Patent No. 6660846
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Caenorhabditis elegans
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Matches 107; Conservative
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US-09-178-093B-1
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324 FWLIDFANACIAVHLIGAYQVFAQPIFQFVEKKCNRNYPDNKFITSEYSVNVPFLGKFNI 383
                                                                                                                                                                                                     272 IGMVLPLENKMKDPRKFPLILYLGMVIVTILYISLGCLGYLQFGANIQGSITLN---LPN 328
                                                                                    329 CWLYQ-----SVKLLYSIGIFFTYALQF-----YVPAEIIIPFFVSRAPEHCELVV 374
                                                                                                                                                                       375 DLF---VRIVLYCLICILAILIPRLDLVISLVGSVSSSALALIIPPLLEVTTFYSEGMSP 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FROMMER, Wolf-Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR AN AMINO ACID
TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA, YEASTE
TITLE OF INVENTION: CONTAINING A TRANSPORTER AND THEIR USE
NUMBER OF SEQUENCES:
ADDRESSE: Ostrolenk, Faber, Gerb & Soffen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,939
FILING DATE:
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20.0%; Pred. No. 1.7e-13;
tive 81; Mismatches 221;
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1180 Avenue of the Americas
                                                                                                                                                                                                                                                                                            444 RWIALKTMCYVCLIVSLLAAAGSIAG 469
                                                                                                                                                                                                                                                                432 LTI-----FKDALISILGFVGFVVG 451
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PRIOR APPLICATION DATA:
RIDING DATE: 05-JAN-1995
FILING DATE: 05-JAN-1995
APPLICATION WUMBER: US 08/007,636
FILING DATE: 21-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 10036-8403
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Floppy FC COMPATIBLE
TOTAL SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08964939
Patent No. 6245970
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
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(212) 382-0888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meilman, Edward A. REGISTRATION NUMBER: 24,
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                              Wolf-Bernd
DNA SEQUENCES FOR AN AMINO ACID
TRANSPORTER, PLASMIDS, BACTERIA, YEASTS AND PLANTS
CONTAINING A TRANSPORTER AND THEIR USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: DATE: DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,512A
FILING DATE: 05-JAN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/007,636
FILING DATE: 21-JAN-1993
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                            APPLICANT: FROMMER, Wolf-Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR AN AMINO:
TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTITILE OF INVENTION: CONTAINING A TRANSPORTER AN NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Ostrolenk, Faber, Gerb & Soffen STREET: 1180 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-107
TELECOMMUNICATION INFORMATION:
                                                                                                                              Sequence 2, Application US/08362512A Patent No. 5719043 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 382-0700
(212) 382-0888
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INFORMATION FOR SEQ 1D NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
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Best Local Similarity 20.0%
Matches 101; Conservative
506 SGFVHSLEGLIE 517
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APPLICANT: Bougueleret, L.
APPLICANT: Jobert, S.
TITLE OF INVENTION Complementary DNA's Encoding Proteins with Signal Peptides
FILE REPERENCE: GENNSET.050CP3
CURRENT FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                                                                                                                                                     124
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                                                                                                                                                                                                                                          8 NEDYHDYSSTDVSPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGNIGTGLLG
                                                                                                                                                Length 485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 KVQLC----GVAQYGN-----LIGVTVGYTITASISLVAVGK-
                                                                                                                                                   DB 2;
                                                                                                                                                8.7%; Score 215.5; DB 2;
.larity 20.0%; Pred. No. 1.7e-13;
Conservative 81; Mismatches 221;
           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-854-774-2
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; Patent No. 6548633
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APPLICANT: Dumas Milne Edwards,
LENGTH: 485 amino
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SOFTWARE: Patent.pm
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ORGANISM: Homo Sapiens
FEATURE:
                                                                                                                                                                        Local Similarity
nes 101; Conserv
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DNA SEQUENCES FOR AN AMINO ACID
TRANSPORTER, PLASMIDS, BACTERIA, YEASTS AND PLANTS
CONTALNING A TRANSPORTER AND THEIR USE
60 LAWAIAQLGWIAGTSILLIFSFITYFTSTWLADCYRAPDPVTGKRNYTYMDVVRSYLGGR 119
                                                                                                                                                                               269 TLRSSPAENKAM--KRASLV---GVSTTTFFYILCGCIGYAAFGNNAPGDFLTDFGFFEP 323
                                                                                                                                                                                                                                                                                                                                                                                                                                 CWLYQ-----SVKLLYSIGIFFTYALQF-----YVPAEIIIPFFVSRAPEHCELVV 374
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                                                                                                      120 KVQLC----GVAQYGN-----LIGVTVGYTITASISLVAVGK-----SNCFHDK 159
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                                                                                                                                                   185 TVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANI-----
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UTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerb & Soffen
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrolenk, Faber, Gerb & STREET: 1180 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 24,735
REFRENCE/DOCKET NUMBER: P/951-107
TELECOMMUNICATION:
TELEPHONE: (212) 382-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/964,939
FILING DATE: 1998-05-28
APPLICATION NUMBER: US 08/007,636
FILING DATE: 21-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 RWIALKTMCYVCLIVSLLAAAGSIAG 469
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-854-774-2; Sequence 2, Application US/09854774; Patent No. 6809233; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 382-0888
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TITLE OF INVENTION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS. TITLE OF INVENTION: NCCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NCCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ. ID NOS: 28208
SEQ. ID NO 20815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 DWSNNSVFDE--TSELLPTLSRV-STKRHSFSLITGNSTAAQTIFNSINTLIGIGMLSLP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 LAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTVMYGLESSPC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 TNNCHNNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITM--LVSLVM 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VFVLSLLP-----LSMLSIFSLLGIISTVGIILSVF 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 INSILCILMGILPISKLPLVTKPİITSYBNIFGITAKYV-----KLDENGKLTDTYGPT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 RVFSTLSFCCVLLISALLLTSFGKLVAFLRSAICDTVCLTLPLL----FYLKLNRSSVG 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.2%; Score 202.5; DB 2;
21.3%; Pred. No. 3.7e-12;
tive 76; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09370253
; Patent No. 6165792
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Amino Acid Transporters
; FILE REFERENCE: BB-1200
; CURRENT APPLICATION NUMBER: US/09/370,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429 MSPLTIFKDALISILGFVGFVVGTYEAL 456
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                 Sequence 20815, Application US/09248796A Patent No. 6747137 GENERAL INFORMATION: APPLICANT: Keith Weinstock et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 IYQFIVQRIPDPSHLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 108; Conservative
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Best Local Similarity
JS-09-248-796A-20815
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US-09-370-253-10
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Faquence 20813, Application US/09248796A

Faquence 20813, Application US/09248796A

Faquence 20813, Application US/09248796A

Fatent No. 6747137

GENERAL INFORMATION:

FATURE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/248, 796A

CURRENT FILING DATE: 1999-02-12

FRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

FRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

LENGTH: 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 IHLLKGNIGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSF 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GLTTTIGRF 277
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                                                                                                                                                                                                                        VSRYVPVKHATFFNLCSITYPHL---SVVFDFAIAVOCFGCAVSYLVLIRDLMPTI----
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                                                                                           8.2%; Score 203.5; DB 2; Length 108; 48.4%; Pred. No. 3.4e-13; live 16; Mismatches 23; Indels 9
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                                                                                                                                                                                                                                                                                                                         : | | | : | : | | | : | CGTYITVEEIIYPTPKVVAGTPQSPFLNLNSTC 102
                                                                                                                                                                                                                                                                                                VGTYEALYELIQPS------NAPIF-INSTC 473
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ORGANISM: Candida albicans
                                                                                                                       Best Local Similarity 48.4
Matches 45; Conservative
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Best Local Similarity
Matches 91; Conserv
; NAME/KEY: SIGNAL
; LOCATION: -28..-1
US-09-599-360B-109
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                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                     92 EMVP--GKRFDRYHELGQHAFGDKLGLWI------VVPQQLIV-EVGVNIVYMVTGG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                             164 DNFKQVIEAANGTTNNCHNNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : | :: | :: | :: | 189 AAVMSLSYSTIAMGASVDKGKMVDVDYNLRATTTPGKVFGFFGALGEVAFAYAGHNVVLE 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 WLYQSVKL---LYSIGIFFTYALQFYVPABILIPFFVSRAPEHCELVVDLFVRTVLVCLT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 WLISTANMMVVIHVIGSYQIYAMPVFDMIETVL---VKKLKFPPGLTLRLIARTLYVAFT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387 CILAILIPRLDLVISLVGSVSSSALALIIPPLLEVTTFYSEGMSPLTIFKDALISILGFV 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANITMLVSLVMIYQFIVQR----IPDPSHLPLVAPWKTYPLF--FGTAIFSFEGIGMVLP 277
                                                                                                                                                                                                                                                                                                                33 SRNAKWWYSAFHNVTAMVGAGVLSLPYAMSELGWGPGIAVLVISWVITLYTLWQMVE-MH 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43308
LENGTH: 150
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                                                                                                                                                                                                             Length 447;
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                                                                                                                                                                                                             Query Match 8.0%; Score 197; DB 2; Length 447
Best Local Similarity 21.3%; Pred. No. 1.2e-11;
Matches 93; Conservative 84; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.9%; Score 196; DB 2; Length 15 Best Local Similarity 35.5%; Pred. No. 3.2e-12; Matches 43; Conservative 24; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa means any amino acid US-09-270-767-43308
CURRENT FILING DATE: 1999-08-09
BARLIER APPLICATION NUMBER: 60/097,222
EARLIER FILING DATE: August 20, 1998
NUMBER OF SEQ ID NOS: 18
SECTIMARE: Microsoft Office 97
LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 43308, Application US/09270767; Patent No. 6703491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447 GFVVGTYEALYELIQPS 463
                                                                                                                                                    ORGANISM: Triticum aestivum US-09-370-253-10
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                                                                                                                                    TYPE: PRT
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73 KNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTVMYGLESSPCSWL 132
                                                                                                                            104 HFCRRLNKSFVDYGDTVMYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 DNPKO---VIEAANGTTNNCHNNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 SLLANITMLVSLVMIYQFIVQ--RIPDPS-HL-PLVAPWKTYPLF--FGTAIFSFEGIGM 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 VLPLE----NKMKDPRKFPLI--LYLGMVIVTILYISLGCLGYLQFGANIQGS--ITLNL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 PNCWLY---QSVKLLYSIGIFFTYALQFYVPAEIIIPFFVSRAPEHCELVVDLFVRTVLV 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | : ::: | : | | : | | : | 306 PK-WLIALANMMVVIHVIGSYQIYAMPVFDMIETVL---VKKLRFPPGLTLRLIARTLYV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 AFTMPIAITFPFFGGLLGFFGGRAPAPTTYFLPCIMWLAIYKPRRFS-LSWFTNWICIIL 420
22 YPTTLELTTPTKSANGSNDDYDPHQHREL--KNPTTNFQTFAHFLKASVGTGVLAMPSAF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 EMVP--GKRFDRYHELGQHARGEKLGLMI------VVPQQLVV-EVGVNIVYMVTGG
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09370253
; Patent No. 6165792
; GENERAL INPORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Amino Acid Transporters
; TITLE OF INVENTION: Amino Acid Transporters
; FILE REFRENCE: BB-1200
; CURRENT APPLICATION NUMBER: US/09/370,253
; CURRENT FILING DATE: 1999-08-09
; EARLIER FILING DATE: August 20, 1998
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Microsoft Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-370-253-6
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RESULT 15 US-09-640-419C-24

14 YSST-DVSPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGNIGTGLLGLPLAV

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APPLICANT: LALLANT Created APPLICANT: Created APPLICANT: LALLANT Created APPLICANT: LALLANT: 
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Best Local Similarity 20.7%; Pred. No. 1.4e-10;
Matches 82; Conservative 79; Mismatches 188; Indels 48; Gaps
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; ORGANISM: Arabidopsis thaliana
US-09-640-419C-24
                                     Parent No. 6630615
GENERAL INFORMATION:
APPLICANT: Bidney, Dennis L
APPLICANT: Crasta, Oswald R
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Search completed: August 24, 2006, 01:26:34 Job time : 51 secs

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Best Local Simi
Matches 476;
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Sequence 7, Appli
Sequence 7, Appli
Sequence 3076, Ap
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8, Appli
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2, Appli
7, Appli
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                                                                       (without alignments)
1191.839 Million cell updates/sec
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: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

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:: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

:: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

:: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

:: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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                                                                                                       US-10-679-362-2
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1 MSTQRLRNEDYHDYSSTDVS......YELIQPSNAPIFINSTCAFI
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                                                             August 24, 2006, 01:25:54; Search time 185 Seconds
GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-080-334-22

US-10-080-334-20

US-09-805-456-7

US-10-080-334-137

US-10-094-749-3076

US-10-094-749-3076

US-10-080-334-138

US-10-225-810-18

US-10-225-810-19

US-10-225-810-19

US-10-35-810-14

US-10-35-810-14

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US-10-35-810-22

US-10-25-810-22

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| Sequence 52, Appl | Sednence 139, App | Sequence 23, Appl | Sequence 22, Appl | Sequence 10, Appl | Sequence 3609, Ap   | Sequence 34, Appl | Sequence 26835, A   | Sequence 141, App | Sequence 4, Appli | Sequence 5, Appli | Sequence 4, Appli | Sequence 5, Appli | Sequence 26193, A   | Sequence 31110, A   | Sequence 140, App | Sequence 5, Appli | Sequence 5, Appli |
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| US-11-043-889-52  | US-10-080-334-139 | US-10-168-651-23  | US-10-755-889-22  | US-10-415-378-10  | US-10-108-260A-3609 | US-10-225-810-34  | US-11-097-143-26835 | US-10-080-334-141 | US-09-805-456-4   | US-09-805-456-5   | US-10-679-362-4   | US-10-679-362-5   | US-11-097-143-26193 | US-11-097-143-31110 | US-10-080-334-140 | US-10-291-737-5   | US-10-365-564-5   |
| 9.                | 4                 | 4                 | 4                 | 4                 | 4                   | 4                 | 9                   | 4                 | ٣                 | m                 | 4                 | 4                 | 9                   | v                   | 4                 | 4                 | 4                 |
| 485               | 504               | 476               | 476               | 443               | 369                 | 482               | 482                 | 504               | 404               | 404               | 404               | 404               | 483                 | 486                 | 165               | 404               | 404               |
| 50.9              | 50.9              | 50.7              | 50.7              | 40.1              | 39.4                | 35.1              | 35.1                | 35.1              | 34.9              | 34.9              | 34.9              | 34.9              | 34.9                | 34.9                | 34.7              | 34.5              | 34.5              |
| 1255.5            | 1255.5            | 1252.5            | 1252.5            | 989.5             | 972.5               | 998               | 998                 | 998               | 861               | 861               | 861               | 861               | 861                 | 861                 | 857               | 853               | 853               |
| 28                | 59                | 30                | 31                | 32                | 33                  | 34                | 32                  | 36                | 37                | 38                | 39                | 40                | 41                  | 42                  | 43                | 44                | 45                |

## ALIGNMENTS

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APPLICANT: WEI, Ming-Hui
APPLICANT: WEI, Ming-Hui
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLES THEREOF
FILE REFERENCE: CLOOLO62
CURRENT PELLING NUMBER: US/09/805,456
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTHARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 1.7e-217;
iive 0; Mismatches 0;
Sequence 2, Application US/09805456 Publication No. US20030170778A1 GENERAL INFORMATION:
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                                                                                                                                           ; Score 2469; DB 4;
; Pred. No. 1.7e-217;
0; Mismatches 0;
CURRENT FILING DATE: 2003-10-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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Gerlach, Valerie
Spaderna, Steven K
Zerhusen, Bryan D
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Spytek, Kimberly A
Vernet, Corine A. M.
Malyankar, Uriel M
Guo, Xiaojia
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100.0%;
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Casman, Stacie J
Boldog, Ferenc L
Furtak, Katarzyna
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Shenoy, Suresh G
                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 476; Conservative
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                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20040146887A1
GENERAL INFORMATION:
APPLICANT: WEL, Ming-Hui
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO01062CON
CURRENT APPLICATION NUMBER: US/10/679,362
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                                                                                                                                                                                                                  Using Tramdorin
                                                                                                                                                                                              APPLICANT: Bermingham, Jr., John R.
TITLE OF INVENTION: Tramdorins and Methods of
FILE REFERENCE: McLaugh-07165
CURRENT APPLICATION WUMBER: US/10/225,810
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.2
                                                                                                                                              ; Sequence 21, Application US/10225810; Publication No. US20030157512A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 476; Conservative
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ORGANISM: Homo sapiens
                                                                                                                   RESULT 2
US-10-225-810-21
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                                                                                                                                                                                                                                                                                                                                  LENGTH: 476
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                                                  FFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLDLVISLVGSVSSSALALIIPPLLE
                                                                                                                                  421 VTTFYSEGMSPLTIFKDALISILGPVGFVVGTYEALYELIQPSNAPIFINSTCAFI 476
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;
APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;
APPLICANT: GREENE, Barrie D.; SANJANWALA, Madhu S.;
APPLICANT: GREENE, Barrie D.; SANJANWALA, Madhu S.;
APPLICANT: ARVIZU', Chandra S.; GANDHI, Ameena R.;
APPLICANT: ARVIZU', Chandra S.; GANDHI, Ameena R.;
APPLICANT: MALLA, Mariaher K.; YAO, Monique G.; YANG, Junming;
APPLICANT: WALLA, Nariaher K.; AU-YOUNG, Janice;
APPLICANT: WALLA, Preed!, ELLIOTT, Vick! S.; NGUYEN, Danniel B.;
APPLICANT: WALSH, ROGGETICK T.; RAMKUWAR, Jayalaxmi;
APPLICANT: WALSH, PREED! T. I.U, DYUNG AIN MIN, AZIMZI, Yalda;
APPLICANT: WALSH, PREED! SELLIOTT, Vick! S.; NGUYEN, Danniel B.;
APPLICANT: TA, Yumisu, Pachicant J., Preed!, ELLIOTT, Vick! S.; NGUYEN, Bark L.;
APPLICANT: DAS, Debopriya; POLICKY, Jennifer L.
TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
FILE REFERENCE: PI-O149 USN
CURRENT APPLICATION NUMBER: US 60/216,547
PRIOR PELLING DATE: 2000-07-07
PRIOR PELLING DATE: 2000-07-07
PRIOR PELLING DATE: 2000-07-07
PRIOR PELLING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-24
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Pred. No. 2.6e-211;
0; Mismatches 2; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040053258A1 7476747CD1
US-10-332-447-8
                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/10332447; Publication No. US20040053258A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local S
Matches 474
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                INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 MSTQRLRNEDYHDYSSTDVSPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKGN
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Pred. No. 1.2e-216;
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99.8%; Pred. No. 1...
0; Mismatches
TITLE OF INVENTION: Proteins, Polynucleotides TITLE OF INVENTION: Using the Same FILE BERERBNCE: 21402-275
CURRENT APPLICATION NUMBER: US/10/080,334
CURRENT FILING DATE: 2002-02-21
PRIOR FILING DATE: 2001-09-17
PRIOR PLING DATE: 2001-09-17
PRIOR PLING DATE: 2001-09-17
PRIOR FILING DATE: 2001-08-13
PRIOR FILING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PELING DATE: 2001-08-13
PRIOR PELING DATE: 2001-08-13
PRIOR PELING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/278,796
PRIOR PELING DATE: 2001-04-04
PRIOR PILING DATE: 2001-04-04
PRIOR PILING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-10
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PRIOR PELICATION NUMBER: 60/276,400
PRIOR PELING DATE: 2001-03-10
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Best Local Similarity 99.8
Matches 475; Conservative
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APPLICANT: WEI, Ming-Hui
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: WICLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001062
CURRENT FILLNG APPLICATION NUMBER: US/09/805,456
CURRENT APPLICATION NUMBER: 2001-03-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
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larity 97.5%; Pred. No. 5.8e-211;
Conservative 0; Mismatches 0; Indels 1:
              PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/291,765
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 388
SOFTWARE: PATCHIN VEY: 2.1
SEQ ID NO 20
LENGTH: 500
TYPE: PRI
APPLICATION NUMBER: 60/286,548
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                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-080-334-20
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Matches 472; Conserv
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APPLICANT: Spaderna, Steven K
APPLICANT: Spaderna, Steven K
APPLICANT: Schusen, Bryan D
ITILE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
ITILE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
ITILE OF INVENTION: Using the Same
FILE REFERENCE: 21402-275
CURRENT APPLICATION NUMBER: 05/270,523
PRIOR APPLICATION NUMBER: 60/222,712
PRIOR APPLICATION NUMBER: 60/311,980
PRIOR FILING DATE: 2001-09-17
PRIOR PELLING DATE: 2001-10-13
PRIOR PELLING DATE: 2001-10-140
PRIOR FILING DATE: 2001-10-180
PRIOR PELLING DATE: 2001-10-180
PRIOR PELLING DATE: 2001-10-180
PRIOR PELLING DATE: 2001-10-180
PRIOR PELLING DATE: 2001-03-26
PRIOR PELLING DATE: 2001-03-26
PRIOR PELLING DATE: 2001-03-16
PRIOR PELLING DATE: 2001-03-16
PRIOR PELLING DATE: 2001-03-16
PRIOR PELLING DATE: 2001-03-18
PRIOR PELLING DATE: 2001-03-18
PRIOR PELLING DATE: 2001-03-18
PRIOR FILING DATE: 2001-03-18
                                            ILYISLGCLGYLQFGANIQGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIP 360
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                                                                                                                                       FFVSRAPEHCELVVDLFVRTVLVCLT
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Padigaru, Muralidhara
Liu, Xiaohong
Baumgartner, Jason C.
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Casman, Stacie J
Boldog, Perenc L
Furtak, Katarzyna
Tchernev, Velizar T
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Shenoy, Suresh G
Kekuda, Ramesh
Spytek, Kimberly A
Vernet, Corine A. M.
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Guo, Xiaojia
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Gerlach, Valerie
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61 IGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTV 120
                               QRIPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVT 300
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Pred. No. 1.9e-194;
1; Mismatches 1;
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APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTAGI
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAGHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: VOSHIKAWA, MOTOTUKI
APPLICANT: NAGAHRI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350, 435
PRIOR APPLICATION NUMBER: 50/350, 435
PRIOR APPLICATION NUMBER: 57 2001-328381
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3076, Application US/10094749; Publication No. US20030219741A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUGIYAMA, TOMOYASU OTSUKI, TETSUJI WAKAMATSU, AI SATO, HIROYUKI ISHII, SHIZUKO YAMAMOTO, JUN-ICHI ISONO, YUUKO
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90.8%;
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APPLICANT: SUGIYAMA, TOMOX
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: YAMAMOTO, JUN-J
APPLICANT: YAMAMOTO, JUN-J
APPLICANT: ISONO, YUUKO
APPLICANT: ISONO, YUUKO
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US-10-094-749-3076
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Best Local Simil
Matches 432; C
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SEQ ID NO 3076
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Publication No. US20040146887A1

GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui
TITLE OF INVENTION:
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
GURRENT APPLICATION NUMBER: US/10/679,362
CURRENT FILING DATE: 2003-10-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASLSEQ for Windows Version 4.0
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                                                                                             Length 476;
                                                                                        94.1%; Score 23.2.94.5%; Pred. No. 3.3e-204; Pred. No. 3.4-204; Indels 17; Indels ive 9; Mismatches 17; Indels
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                                                                                                               Best Local Similarity 94.5
Matches 450; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Human
US-10-679-362-7
                             TYPE: PRT
ORGANISM: Human
                                                    ; ORGANISM: H1
US-09-805-456-7
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 SEQ ID NO 7
                                                                                               Query Match
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US-10-080-334-138
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Wernet, Corine A. M.
APPLICANT: Wernet, Corine A. M.
APPLICANT: Gusev, Uselia M.
APPLICANT: Gassian, Stacie J.
APPLICANT: Gassian, Stacie J.
APPLICANT: Furtak, Katarzyna
APPLICANT: Furtak, Katarzyna
APPLICANT: Padigatu, Murslidhara
APPLICANT: Padigatu, Murslidhara
APPLICANT: Baugastner, Jason C.
APPLICANT: Baugastner, Jason C.
APPLICANT: Spaderna, Steven K
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Publication No. US20040002584A1
GENERAL INFORMATION:
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Shenoy, Suresh G
Kekuda, Ramesh
Spytek, Kimberly A
Verner, Corine A. M.
Malyankar, Uriel M
Guo, Xiaojia
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181 HNNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIV 240
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Pred. No. 1.9e-194;
1; Mismatches 1;
                  PRIOR APPLICATION NUMBER: 60/276,677
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/270,220
PRIOR APPLICATION NUMBER: 60/274,295
PRIOR PELING DATE: 2001-02-10
PRIOR PELING DATE: 2001-03-08
PRIOR PELING DATE: 2001-03-08
PRIOR PELING DATE: 2001-03-08
PRIOR PELING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/286,548
PRIOR PELING DATE: 2001-04-25
PRIOR PELING DATE: 2001-04-25
PRIOR PELING DATE: 2001-04-25
PRIOR PELING DATE: 2001-04-25
PRIOR PELING DATE: 2001-03-176
PRIOR PELING DATE: 2001-02-17
PRIOR PELING DATE: 2001-02-17
PRIOR PELING DATE: 2001-02-17
PRIOR PELING DATE: 2001-02-17
PRIOR PELING DATE: 2001-02-18
PRIOR APPLICATION NUMBER: 60/276,400
PRIOR PELING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 388
NUMBER OF SEQ ID NOS: 388
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FILING DATE: 2001-04-04
APPLICATION NUMBER: 60/276,677
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Best Local Similarity 90.8%;
Matches 432; Conservative 1
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US-10-080-334-137
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61 IGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSFVDYGDTV
                           60 IGTGLLGLPLAVKNAGLLLGPLSLLVIGIVAVHCMGILVKCAHHLCRRLNKPFLDYGDTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 41, Application US/10225810
Publication No. US20030157512A1
Publication No. US20030157512A1
Publication No. US20030157512A1
APPLICANT: Bermingham, Jr., John R.
TITLE OF INVENTION: Trandorins and Methods of Using Trandorin:
CURRENT APPLICATION NUMBER: US/10/225,810
CURRENT APPLICATION NUMBER: US/10/225,810
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.2
SEQ ID NO 41
LENGTH: 475
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US-10-225-810-41
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US-10-225-810-41
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APPLICANT: Garlach, Valerie
APPLICANT: Sandarna, Steven K
APPLICANT: Sandarna, Bryan D
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE OF INVENTION: Using the Same
FILE SPEERSNCS: 21402-213
FRIOR APPLICATION NUMBER: US/10/080,334
CURRENT TILING DATE: 2001-02-21
FRIOR APPLICATION NUMBER: 60/320,122
FRIOR APPLICATION NUMBER: 60/320,122
FRIOR APPLICATION NUMBER: 60/320,122
FRIOR FILING DATE: 2001-08-13
FRIOR FILING DATE: 2001-08-13
FRIOR FILING DATE: 2001-08-13
FRIOR FILING DATE: 2001-08-13
FRIOR FILING DATE: 2001-08-14
FRIOR FILING DATE: 2001-08-16
FRIOR FILING DATE: 2001-08-16
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                Patturajan, Meera
Gangolli, Esha A
Padigaru, Muralidhara
                                                                                                                                                          Gusev, Vladimir y
Casman, Stacie J
Boldog, Perenc L
Furtak, Katarzyna
Tchernev, Velizar T
                                                                                                                                                                                                                                                                                                                                                                             Baumgartner, Jason C.
Gerlach, Valerie
                                                               Spytek, Kimberly A
Vernet, Corine A. M.
Malyankar, Uriel M
Guo, Xiaojia
                        Suresh G
Ramesh
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ORGANISM: Rattus norvegicus
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Best Local Similarity 85.77
Matches 408; Conservative
                                                                                                                                                                                                                                                                                                                                                          Liu, Xiaohong
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Sequence 4, Application US/1036564;
publication No. US2003014362341
| GENERAL INFORMATION:
| TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
| TITLE OF INVENTION: WUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
| TITLE OF INVENTION: WULL AND USES THEREOF
| TITLE OF INVENTION: WUMBER: US/10/365,564
| TITLE OF INVENTION: WUMBER: US/10/365,564
| TITLE OF INVENTION: WUMBER: US/10/365,564
| PRIOR APPLICATION WUMBER: US/02/38
| PRIOR APPLICATION WUMBER: US/02/458
| PRIOR PILING DATE: 2000-02-13
| PRIOR FILING DATE: 2000-12-12
| PRIOR FILING DATE: 2000-12-12
| PRIOR FILING DATE: 2000-12-12
| WUMBER OF SEQ ID NOS: 6
| SOFTWARE: FastSEQ for Windows Version 4.0
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: CLO01017-CON CURRENT APPLICATION NUMBER: US/10/291,737

PRIOR APPLICATION NUMBER: US 09/822,859

PRIOR FILING DATE: 2001-04-02

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86.0%; Pred. No. 1.1e-166;
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77.5%; Score 1914; WE Best Local Similarity 86.0%; Pred. No. 1.16-Matches 363; Conservative 33; Mismatches
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ORGANISM: Human
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          300 VLYISLGSLGYLQFGADIKGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVAAEIIIP 359
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                                                                                                                                     VITFYSEGMSPLTIFKDALISILGFVGFVVGTYEALYELIQPSNAPIFINSTCAFI 476
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.6%; Score 2137.5; DB 4
85.9%; Pred. No. 4.2e-187;
ive 32; Mismatches 34;
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TITLE OF INVENTION: Trandorins and Methods
FILE REFERENCE: McLaugh-07165
CURRENT APPLICATION NUMBER: US/10/225,810
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
                                                                                                                                                                                                                                                                                  ; Sequence 18, Application US/10225810; Publication No. US20030157512A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10291737
Publication No. US20030087299A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity 85.9
409; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Mus musculus
US-10-225-810-18
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US-10-225-810-18
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                                             Query Match 77.5%; Score 1914; DB 4; Length 422; Best Local Similarity 86.0%; Pred. No. 1.1e-166; Matches 363; Conservative 33; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Seafch completed: August 24, 2006, 01:29:45
Job time : 186 secs
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Human
US-10-365-564-4
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US-10-505-928-42

Sequence 42, Application US/10505928

Publication No. US2006008833A1

GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research et al.

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866

SEQ ID NO 42
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US-11-056-355B-75679
US-11-056-355B-75678
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US-11-056-355B-96649
US-11-056-355B-3644879
US-11-056-355B-4888
US-11-056-355B-8881
US-11-056-355B-8581
US-11-056-355B-8581
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Best Local Similarity 52.0%
Matches 254; Conservative
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Sequence 3609, Ap
Sequence 369, App
Sequence 3701, App
Sequence 3701, A
Sequence 49196, A
Sequence 53550, A
Sequence 53580, A
Sequence 53580, A
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32686, A
36917, A
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105676,
116915,
116914,
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977.303 Million cell updates/sec
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/EMC_celerra_SID63/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/EMC_celerra_SID63/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/EMC_celerra_SID63/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/EMC_celerra_SID63/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/EMC_celerra_SID63/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
/EMC_celerra_SID63/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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                           GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-11-293-697-3609
US-10-953-349-368
US-10-953-349-368
US-10-449-902-37011
US-10-449-902-53550
US-10-449-902-53486
US-10-449-902-53550
US-10-449-902-53560
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US-10-449-902-53560
US-11-0449-902-36917
US-11-056-355B-116916
US-11-056-355B-116916
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US-11-056-355B-116916
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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2469
1 MSTQRLRNEDYHDYSSTDVS.
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65 77

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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: BENCONDED THERBY
FITLE OF INVENTION: BENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                                                                                                    92 LDSFNAGISKIGSFGD-----LGFAVCGSL------GRIVVDLFIILSQAGFCVGYLIFI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 ---FGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVTILYISLGCLGYLQFGANI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 MGPISLLIIGIVAVHCMGILVKCAHHFCRRLNKSF-----VDYGDTVMYGLESSPCSW 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 ADNFKQVIEAANGTT-NNCHNNETVILTPT-------MDSRLYMLSFLPFL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 OGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIPFFVSRAPEHCELVVDLFV 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 MDIITANLGAGLUSTVVQLGLCINLFFTFPLMMNPVFEIVERRF-SRG-----MYSAWL 351
                                                                                                                                                                                                                                                                                                                    50 FOTLIHLLKGNIGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 ------GTTLANLSDPE----SPTSLRHQFTRLGSEFLGVSSKSLYIWGCFPFQ 184
                                                                                                                                                                                                                                                                                                                                            110 NKSF-----VDYGDTVMYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 VLLVFIRNLRALSIFSLLANI----TMLVSLVMIYQFIVQRIPDPSHLPLVAPWKTYPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 LYGMGVAVYSFEGVGMVLPLESEMKDKDKFGKVLALGMGFISLIYIAFGILGYLAFGEDT
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llarity 32.0%; Pred. No. 2.4e-26;
Conservative 60; Mismatches 143;
                                                                                                                                                                                                                                      Query Match 18.9%; Score 465.5; DB 6; Best Local Similarity 32.4%; Pred. No. 8.2e-31; Matches 143; Conservative 66; Mismatches 155;
TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579PUS2 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE: Patentin version 3.3 SEQ ID NO 368 LENGTH: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 369, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 LISILGFVGFVVGTYEALYEL 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 AIVVLGVVLAVSGTWSSLSEI 431
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Best Local Similarity
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
                        466
                                                                                                        174 NGTTNNCHNNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITMLVSLV 233
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                                                                                  415 IPPLLEVTTFYSEGMSPLTIFKDALISILGFVGFVVGTYEALYELIQPS-----NAP
    AEIIIPFFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLDLVISLVGSVSSSALALI
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                                                                                                                                                                                                                                                                                         ; Sequence 3609, Application US/11293697; Publication No. US20060105376A1
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELLX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REPERENCE: H1-A0106
; GURRENT RPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; RRIOR APPLICATION NUMBER: US/10/108,260
; RIUNGER OF SEQ ID NOS: 5458
; SÖFTWARE: PatentIn Ver. 2.1
; EQUID NO 3609
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Publication No. US20060107345A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: National Institute of Physical Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MAG-AD20571-US
CURRENT APPLICATION NUMBER: UP 2002-203269
PRIOR FILING DATE: 2003-05-39
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
                                  GMVLPLENKMKDPRKFPLILYLGMVIVTILYISLGCLGYLQFGANIQGSITLNLPNCWLY
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ORGANISM: Oryza sativa
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APPLICANT: National Institute of Payrology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR PELICATION NUMBER: UP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR APPLICATION NUMBER: UP 2002-18-11
NUMBER OF SEQ ID NOS: 56791
SEQ ID NO 37011
S YDHPKIASFGD-----LGAAVC-----GPAGRHVVDAMLVLSQASFCVGYLIFISNIWA
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                                                                                                                     231 SLVMIYQFIVQRIPDPSHLPLVAPWKTYPLF---FGTAIFSFEGIGMVLPLENKMKDPRK
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Similarity 27.6%; Pred. No. 8e-26;
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Publication No. US20060123505A1
GENERAL INFORMATION:
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; ORGANISM: Oryza sativa
US-10-449-902-37011
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                                                                                                                                                                                                              Sequence 32842, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
450 VGTYEALYELIQPSN 464
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SGTWTSLAQIFSSSD 424
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Best Local Similarity 26.9
Matches 126; Conservative
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ORGANISM: Oryza sativa
US-10-449-902-32842
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LENGTH: 422
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Sequence 53550, Application US/10449902 Publication No. US20060123505A1 GENERAL INFORMATION:

US-10-449-902-53550

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206 VWLAKPPPVFAFGGLSAILYGIGVSVYAFEGIGMVLPLEAEAANKKKFGTTLGLSMGFIA 265
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
TILE REPERINCE: POLA-AD20SY1-US
FILE REFERENCE: MOA-AD20SY1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR FILING DATE: 2003-05-29
PRIOR PLING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 53550
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APPLICANT: National Institute of Physical Advancement Institution.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: Bio-oriented Fechnology Research Advancement Institution.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-AA20571-US
CURRENT PELING DATE: 2003-05-29
CURRENT FILING DATE: 2003-05-29
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-30369
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Publication No. US20060123505A1
GENERAL INFORMATION:
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US-10-449-902-53550
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Sequence 370, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: BACOUNDED THERBY
TITLE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 4025-2
SOFTWARE: Patentin version 3.3
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                                                                                                                        1.0 --NKSFVDYGDTVMYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADNFK 167
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                                                                                                                                                227 TMLVSLVMIYQFIVQRIPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPR
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                                                                 347 YALQF---YVPAEIIIPFFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLDLVISLV
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                                           OTLIHLLKGNIGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRRL-
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32.8%; Pred. No. 5.1e-24;
tive 51; Mismatches 131; Indels
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328 NCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIPFFVSRAPEHCELVVDLFVRTVLVCLTC 387
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APPLICANT: Blo-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
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; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
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314 DVLLVLLGLSLAVFGTYTSLLQIFHSSSA 342
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339 AVSGTWSSLSEI 350
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US-10-449-902-32686
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RESULT 13

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APPLICANT: ALEXANDROW, Nickolai
APPLICANT: ALEXANDROW, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: UNGLEDTIDE SEQUENCES AND FOLYPEPTIDES ENCODED THEREBY
TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
TITLE REPERENCE: 2750-1601PUS2
CURRENT APPLICATION NUMBER: US/11/174,307B
CURRENT APPLICATION NUMBER: 06/583,671
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR SEQ ID NOS: 5544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 NNETVILTPTMDSRLYMLSFLPFLVLLVFIRNLRALSIFSLLANITMLVSLVMIYQFIVQ 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 RIPDP--SHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 TILYISLGCLGYLQFGANIQGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIII 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 PFF-----VSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLDLVISLVGSVSSAL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GRRVVDFFLIVTQLGFCCVYFVFLADNFKQVIEAANGTTNNCH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 ERPOSSGCFPKLSHKVRGAEWVGLHSSRIVMVTILSVVASFIPAFGSFISFVGSTVCALL 302
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                                                                                                                                         Institution.
Sequence 36917, Application US/10449902

Sequence 36917, Application US/10449902

Publication No. US20060123505A1

GENERAL INPORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Science.

TITLE OF INVENTION: PULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT APPLICATION NUMBER: US/202-203269

PRIOR APPLICATION NUMBER: UP 2002-203269

PRIOR PILING DATE: 2002-05-30

PRIOR PLING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 56791

SEQ ID NOS: 56791

SEQ ID NOS: 56791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 13.4%; Score 332; DB 6; Length 34 Best Local Similarity 27.6%; Pred. No. 6.8e-20; Matches 96; Conservative 61; Mismatches 145; Indels
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; Publication No. US20060143729A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Oryza sativa
US-10-449-902-36917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 DYGDTVMYGLESSPCSWLRNHAHWGRRVVDFFLIVTQLGFCCVYFVFLADN----FKQV- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 LLGICLFWVGAVDGIGFHATGRVFDLSNLPVT-----IGIFGFGYSGHSVFPNIYS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 KMKDPRKFPLILYLGMVIVTILYISLGCLGYLQFGANIQGSITLNLPNCWLYQSVKLLYS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGIFFT-YAL---QFYVPAEIIIPFFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 TMLVSLVMIYQ-----FIVQRIPDPSHLPLVAPWKTYPLFFGTAIFSFEGIGMVLPLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 STORLRNEDYHDYSST - - DVSPEESPSEGLNNLSSPGSYQRFGQSNSTTWFQTLIHLLKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 SSKPLLSQPVPDKEETILPVNPQSQLKLSVTDLPLP-----EPNLCSFSQSVLNGTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 IEAANGTINNCHNNETVILIPIMDSRLYMLSFLPFLVLLVFIRNLRALSIFS---LLANI
                                                                                                               Fragments and Corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87; Mismatches 188; Indels
                                                                                   APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragment
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR FILING DATE: 2005-02-14
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 105677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.2%; Score 302; DB 7; 25.3%; Pred. No. 2.9e-17;
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OTHER INFORMATION: Ceres Seq. ID no. 13617748
US-11-056-355B-105677
Sequence 105677, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity
Matches 123; Conserv
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                                                                                                                                                                                                                     INFORWATION: GI Number: 50904567; NR Description: putative amino acid INFORMATION: transport protein [Oryza sativa (japonica cultivar-group)] INFORMATION: >gi|41053220|dbj|BAD08181.1| putative amino acid transport protei
                                                                                                                                                                                                                                                                                                                                                      INFORMATION: GI Number: 50915446; NR Description: amino acid INFORMATION: transporter-like [Oryza sativa (japonica cultivar-group)] INFORMATION: 5gi 47497045|dbj|BAD19097.1| amino acid transporter-like [Oryza INFORMATION: sativa (japonica cultivar-group)] sgi 47497767|dbj|BAD19867.1|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: GI Number: 42563873; NR Description: amino acid transporter US-11-174-307B-5170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION: GI Number: 30687791; NR Description: amino acid transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: GI Number: 42563875; NR Description: amino acid transporter
                                                                                                                                     Name: Aa_trans; PFam Description: Transmembrane amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INLPNCWLYQSVKLLYS-IGIFFTYALQFYVPAEIIIPFFVSRAPEHC-----ELVVD 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            376 LFVRTVLVCLTCILAILIPRLDLVISLVGSVSSSALALIIPPLLEVTTFYSEGMSPLTIF 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCAHHFCRRLNKSFVDYGDTVMYGLESSPCSWLRNHAHWGR--RVVDFFLIVTQLGFCCV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 YEVEL-ADNEKQVIEAANGTINNCHNNETVILIPIMDSRLYMLSFLPFLVLL--VFIRNL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RALSIFS---LLANITMLVSLVMI-----YQFIVQRIPDPSHLPLVAPWKTYPLFFG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 TAIFSFEGIGMVLPLENKMKDPRKFPLILYLGMVIVTILYISLGCLGYLQFGANIQGSIT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 IYGFCYSGHSVFPNIYQSMSDRTKFPKALFICFAVCTAIYGSFAIIGYLMFGDKTLSQIT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOSNSTIWFOILIHLLKGNIGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHC--MGILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GEAAFGRIGRLIISIILYTELYSYCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 EFIILEGDNMTSIFPDVNINLFGIH------VDSK-HFFGVLTALVVLPTVWLRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.9%; Score 318; DB 7; Length 53 25.8%; Pred. No. 1.6e-10; ive 73; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 KDALISILGFVGFVVGTYEALYELI 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 K----HCFESKDGIATYPDI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.8°
Matches 115; Conservative
                                                                                                                                        OTHER INFORMATION: PFam
                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
                                                                                               NAME/KEY: misc feature
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